

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 20:03:04 ; Search time 931 Seconds  
(without alignments)  
10429.414 Million cell updates/sec

Title: US-10-718-264-15

Perfect score: 1767

Sequence: 1 accagcgcacttcggcagc.....agaagtgcgtgaagtatt 1767

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	100.0	1767	16	US-10-682-420-15
2	1767	100.0	1767	16	US-10-682-420-19
3	1767	100.0	1767	16	US-10-409-613-15
4	1767	100.0	1767	16	US-10-409-613-19
5	1767	100.0	1767	16	US-10-442-180-15
6	1767	100.0	1767	16	US-10-442-180-19
7	1629.6	92.2	1768	9	US-09-935-428A-1
8	1629.6	92.2	1768	15	US-10-334-245-1
9	1629.6	92.2	1768	17	US-10-653-849-1
10	1628	92.1	1768	9	US-09-935-428A-11
11	1628	92.1	1768	15	US-10-334-245-11
12	1628	92.1	1768	17	US-10-653-849-11

13	1620	91.7	1768	13	US-10-112-540-1	Sequence 1, Appli
14	1412	79.9	1767	9	US-09-784-962-1	Sequence 1, Appli
15	1412	79.9	1767	9	US-09-884-514-1	Sequence 1, Appli
16	1410.4	79.8	1767	9	US-09-784-962-2	Sequence 2, Appli
17	1410.4	79.8	1767	9	US-09-884-514-2	Sequence 2, Appli
18	1335.4	75.6	1768	9	US-09-784-962-3	Sequence 3, Appli
19	1335.4	75.6	1768	9	US-09-784-962-4	Sequence 3, Appli
20	1335.4	75.6	1768	9	US-09-884-514-3	Sequence 3, Appli
21	1335.4	75.6	1768	9	US-09-884-514-4	Sequence 4, Appli
22	1324.6	75.0	1768	9	US-09-884-514-6	Sequence 6, Appli
23	1219	69.0	1343	9	US-09-935-428A-24	Sequence 24, Appli
24	1219	69.0	1343	15	US-10-334-245-24	Sequence 24, Appli
25	1219	69.0	1343	17	US-10-653-849-24	Sequence 24, Appli
26	1176.4	66.6	1768	15	US-10-314-512-1	Sequence 1, Appli
27	1007.2	57.0	1759	16	US-10-682-420-1	Sequence 1, Appli
28	1007.2	57.0	1759	16	US-10-409-613-1	Sequence 1, Appli
29	1007.2	57.0	1759	16	US-10-442-180-1	Sequence 1, Appli
30	1005.6	56.9	1759	16	US-10-682-420-163	Sequence 163, App
31	1005.6	56.9	1759	16	US-10-442-180-163	Sequence 163, App
32	1005.6	56.9	1759	16	US-10-682-420-5	Sequence 5, Appli
33	1004	56.8	1759	16	US-10-409-613-5	Sequence 5, Appli
34	1004	56.8	1759	16	US-10-442-180-5	Sequence 5, Appli
35	1004	56.8	1759	16	US-09-935-428A-2	Sequence 2, Appli
36	1000.8	56.6	1759	15	US-10-334-245-2	Sequence 2, Appli
37	1000.8	56.6	1759	16	US-10-682-420-164	Sequence 164, App
38	1000.8	56.6	1759	16	US-10-409-613-164	Sequence 164, App
39	1000.8	56.6	1759	16	US-10-442-180-164	Sequence 164, App
40	1000.8	56.6	1759	17	US-10-653-849-2	Sequence 2, Appli
41	1000.8	56.6	1759	17	US-10-682-420-23	Sequence 23, Appli
42	945	53.5	945	16	US-10-682-420-23	Sequence 23, Appli
43	945	53.5	945	16	US-10-409-613-23	Sequence 23, Appli
44	945	53.5	945	16	US-10-442-180-23	Sequence 23, Appli
45	886.4	50.2	1759	9	US-09-784-962-5	Sequence 5, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-682-420-15  
; Sequence 15, Application US/10682420  
; Publication No. US20040062775A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH FIGLET WEIGHT LOSS  
; TITLE OF INVENTION: DISEASE (PWD)  
; FILE REFERENCE: 065691/0176  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: US/10/682,420  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US/09/514,245B  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Type B PWD circovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(111)

Wed Dec 8 12:30:21 2004

```
FEATURE: CDS
NAME/KEY: (115)..(243)
LOCATION: (115)..(243)
FEATURE:
NAME/KEY: CDS
LOCATION: (247)..(267)
FEATURE:
NAME/KEY: CDS
LOCATION: (271)..(360)
FEATURE:
NAME/KEY: CDS
LOCATION: (364)..(417)
FEATURE:
NAME/KEY: CDS
LOCATION: (421)..(447)
FEATURE:
NAME/KEY: CDS
LOCATION: (451)..(471)
FEATURE:
NAME/KEY: CDS
LOCATION: (475)..(510)
FEATURE:
NAME/KEY: CDS
LOCATION: (514)..(516)
FEATURE:
NAME/KEY: CDS
LOCATION: (520)..(729)
FEATURE:
NAME/KEY: CDS
LOCATION: (733)..(753)
FEATURE:
NAME/KEY: CDS
LOCATION: (757)..(759)
FEATURE:
NAME/KEY: CDS
LOCATION: (763)..(804)
FEATURE:
NAME/KEY: CDS
LOCATION: (808)..(861)
FEATURE:
NAME/KEY: CDS
LOCATION: (865)..(984)
FEATURE:
NAME/KEY: CDS
LOCATION: (988)..(1173)
FEATURE:
NAME/KEY: CDS
LOCATION: (1177)..(1233)
FEATURE:
NAME/KEY: CDS
LOCATION: (1237)..(1359)
FEATURE:
NAME/KEY: CDS
LOCATION: (1363)..(1476)
FEATURE:
NAME/KEY: CDS
LOCATION: (1480)..(1737)
FEATURE:
NAME/KEY: CDS
LOCATION: (1741)..(1767)
US-10-682-420-15

Query Match 100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGGCGAGCACTTCGGCAGCACTTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGCGCACTTCGGCAGCGGCGAGCACTTCGGCAGCACTTCAGCAGCAACATGCCAGCA 60
Qy 61 AGAAGATGGAGAGCGGAGCCCAACCCCATAAAGGTGGGTCTTCACCTCTGAATAATC 120
Db 61 AGAAGATGGAGAGCGGAGCCCAACCCCATAAAGGTGGGTCTTCACCTCTGAATAATC 120

121 CTTCCGAAGACGAGCGCAAGAAATAACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
121 CTTCCGAAGACGAGCGCAAGAAATAACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
181 TTGTTGGCGAGGAGGTTAATGAGGAAGACGAAACCTCACTCCAGGGTTCGTAATT 240
181 TTGTTGGCGAGGAGGTTAATGAGGAAGACGAAACCTCACTCCAGGGTTCGTAATT 240
241 TTGTTGAAGAACGAGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCGCTGCCACATCG 300
241 TTGTTGAAGAACGAGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCGCTGCCACATCG 300
301 AGAAACGGAAGAACAGATCAGCAGATAAAGAAATACCTGCAATGAAGAACCACTTAC 360
301 AGAAACGGAAGAACAGATCAGCAGATAAAGAAATACCTGCAATGAAGAACCACTTAC 360
361 TGATGAGTGTGAGCTCCTAGATCTCAGGGAACGAGTACCTGTCTACTGTGTA 420
361 TGATGAGTGTGAGCTCCTAGATCTCAGGGAACGAGTACCTGTCTACTGTGTA 420
421 GTACCTTGTGGAGAGCGGAGTCTGTCACCGTTGCAGAGCAGCACCTGTAAACGTTG 480
421 GTACCTTGTGGAGAGCGGAGTCTGTCACCGTTGCAGAGCAGCACCTGTAAACGTTG 480
481 TCAGAAATTTCCGCGGCTGGCTGAACTTTGAAAGTGAGCGGGAATAATGCAAGCGTG 540
481 TCAGAAATTTCCGCGGCTGGCTGAACTTTGAAAGTGAGCGGGAATAATGCAAGCGTG 540
541 ATTGGAAGACTAATGTACAGTCACTTGTGGGCGCACCTGGTGTGTAAGCAAAATGGG 600
541 ATTGGAAGACTAATGTACAGTCACTTGTGGGCGCACCTGGTGTGTAAGCAAAATGGG 600
601 CTGCTAATTTGCAGACCCCGAAACACACATACCTGGAACCCACCTAGAAACAGTGTGG 660
601 CTGCTAATTTGCAGACCCCGAAACACACATACCTGGAACCCACCTAGAAACAGTGTGG 660
661 ATGGTTACCATGTGTAAGAGTGGTGTATTTGATGACATTTTATGCTGCTGCTCCCTGG 720
661 ATGGTTACCATGTGTAAGAGTGGTGTATTTGATGACATTTTATGCTGCTGCTCCCTGG 720
721 ATGATCTACTGAGACTGTGATCGATATCCATTTACTGTAGAGACTAAAGTGGAACTG 780
721 ATGATCTACTGAGACTGTGATCGATATCCATTTACTGTAGAGACTAAAGTGGAACTG 780
781 TACCTTTTTGGCGCGCAGTATTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
781 TACCTTTTTGGCGCGCAGTATTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
841 CCTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTTCTCTTGGTATTTT 900
841 CCTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTTCTCTTGGTATTTT 900
901 GGAAGATGTCTACAGAACATCCACGGAAGAGGGGCGCAGTTCGTCACTTTCCTCCCT 960
901 GGAAGATGTCTACAGAACATCCACGGAAGAGGGGCGCAGTTCGTCACTTTCCTCCCT 960
961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTA 1020
961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTA 1020
1021 TTTTATTAATTAATTAAGGGTAAAGTGGGGGTCTTTTAAATTAATTAATTAATTAATTA 1080
1021 TTTTATTAATTAATTAAGGGTAAAGTGGGGGTCTTTTAAATTAATTAATTAATTAATTA 1080
1081 ATACATGTGTACACGATATTTGATTTCTGTGCTGATATACCTGTTTGAACGAGTGCC 1140
1081 ATACATGTGTACACGATATTTGATTTCTGTGCTGATATACCTGTTTGAACGAGTGCC 1140
1141 GAGGCGTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT 1200
1141 GAGGCGTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT 1200
```

1201 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260  
1201 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260  
1261 GGAGTGGTAGGAAGGGCTGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGTTC 1320  
1261 GGAGTGGTAGGAAGGGCTGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGTTC 1320  
1321 ATAGGTGAGGGCTGGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGACTGCGAGCC 1380  
1321 ATAGGTGAGGGCTGGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGACTGCGAGCC 1380  
1381 CACTCCCTGTGTCACCTCGGGTATCGGGAGCAGAGCCAGAGATTCACCTTAACTTTCT 1440  
1381 CACTCCCTGTGTCACCTCGGGTATCGGGAGCAGAGCCAGAGATTCACCTTAACTTTCT 1440  
1441 TATCTGTAGTATTCAAAGGGCAGAGCGGGGGTTTGACCCCTCTCTGGGGGAAGAA 1500  
1441 TATCTGTAGTATTCAAAGGGCAGAGCGGGGGTTTGACCCCTCTCTGGGGGAAGAA 1500  
1501 GTCAATTAATTAATGAAATCTCATATGTCACCCGAGAGGGCGCTTCTGACTGTGGTTCG 1560  
1501 GTCAATTAATTAATGAAATCTCATATGTCACCCGAGAGGGCGCTTCTGACTGTGGTTCG 1560  
1561 CTTGACAGTATATCCGAAGTTCGGGAGAGCGGGGTGTTGAAGATGCCATTTTCTTTCT 1620  
1561 CTTGACAGTATATCCGAAGTTCGGGAGAGCGGGGTGTTGAAGATGCCATTTTCTTTCT 1620  
1621 CCAGCGGTAACTGGTGGCGGGGTGACGAGCCAGCGGGCGGGGAGGATCTGGCCAG 1680  
1621 CCAGCGGTAACTGGTGGCGGGGTGACGAGCCAGCGGGCGGGGAGGATCTGGCCAG 1680  
1681 ATGGCTGGGGGGCGGTGCTTCTTCTCGGTAAACGCTCTTGGATAGTCTATCTGA 1740  
1681 ATGGCTGGGGGGCGGTGCTTCTTCTCGGTAAACGCTCTTGGATAGTCTATCTGA 1740  
1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767  
1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767

RESULT 2  
US-10-682-420-19/c  
; Sequence 19, Application US/10682420  
; Publication No. US20040062775A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
; TITLE OF INVENTION: DISEASE (PWD)  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/10/682,420  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: US/10/637,011  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US/09/514,245B  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 19  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Type B PWD circovirus

US-10-682-420-19  
Query Match 100.0%; Score 1767; DB 16; Length 1767;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACCAGCGCATTTCGGCAGCGCAGCCTCCGACAGCAGCCTCAGCAGCAACATGCCACGA 60  
DB 1767 ACCAGCGCATTTCGGCAGCGCAGCCTCCGACAGCAGCCTCAGCAGCAACATGCCACGA 1708  
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 120  
DB 1707 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 1648  
QY 121 CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180  
DB 1647 CTTCCGAAGACGAGCGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 1588  
QY 181 TTGTTGGCAGAGAGGTTAATGAGGAGCAGAACCTCACCTCCAGGGGTTTCGCTAATT 240  
DB 1587 TTGTTGGCAGAGAGGTTAATGAGGAGCAGAACCTCACCTCCAGGGGTTTCGCTAATT 1528  
QY 241 TTGTCAGAGCAGACTTTTAAATAAAGTGAAGTGTATTTGGGTGCCCGCTCCACATCG 300  
DB 1527 TTGTCAGAGCAGACTTTTAAATAAAGTGAAGTGTATTTGGGTGCCCGCTCCACATCG 1468  
QY 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGCAACTTAC 360  
DB 1467 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGCAACTTAC 1408  
QY 361 TGATCGAGTGTGAGCTCCTAGATCTCAGGGCAACAGGAGTGACCTGTCTACTGCTGTA 420  
DB 1407 TGATCGAGTGTGAGCTCCTAGATCTCAGGGCAACAGGAGTGACCTGTCTACTGCTGTA 1348  
QY 421 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTGTGAGAGCAGCAACCTGTAAACGTTTG 480  
DB 1347 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTGTGAGAGCAGCAACCTGTAAACGTTTG 1288  
QY 481 TCAGAAATTTCCGCGGGTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGACGCTG 540  
DB 1287 TCAGAAATTTCCGCGGGTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGACGCTG 1228  
QY 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600  
DB 1227 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 1168  
QY 601 CTGCTAATTTTCAGACCCGGAAACACATCTGGAACCCACCTAGAAAACAGTGTGGG 660  
DB 1167 CTGCTAATTTTCAGACCCGGAAACACATCTGGAACCCACCTAGAAAACAGTGTGGG 1108  
QY 661 ATGGTTACCATGTTGAAGAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGG 720  
DB 1107 ATGGTTACCATGTTGAAGAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGG 1048  
QY 721 ATGATCTACTGAGACTGTGTGATTCGATTCGATTCATTTGATGACTAAGGTGGAACTG 780  
DB 1047 ATGATCTACTGAGACTGTGTGATTCGATTCGATTCATTTGATGACTAAGGTGGAACTG 988  
QY 781 TACCTTTTTTGGCCCCGAGTATTCGATTACAGCAATCAGACCCCGTTTGGATGTGACT 840  
DB 987 TACCTTTTTTGGCCCCGAGTATTCGATTACAGCAATCAGACCCCGTTTGGATGTGACT 928  
QY 841 CTTCAACTCTGTGCCAGCTGTAGAGCTCTTTTATCGGAGGATTACTCTCTTGGTATTTT 900  
DB 927 CTTCAACTCTGTGCCAGCTGTAGAGCTCTTTTATCGGAGGATTACTCTCTTGGTATTTT 868  
QY 901 GGAAGAAATGCTACAGAACAATCCACGAGAGAGGGGGCAGTTCGTACCCCTTCCCCCC 960  
DB 867 GGAAGAAATGCTACAGAACAATCCACGAGAGAGGGGGCAGTTCGTACCCCTTCCCCCC 808  
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATGACTCTTTTATCACTTCCTGAATGGT 1020  
DB 807 CATGCCCTGAATTTCCATATGAATAAATTAATGACTCTTTTATCACTTCCTGAATGGT 748

1021 TTTTATTATTAAAGGTTAACTGGGGGCTTTTAAATTAATTTCTGTAATCTGAC 1080  
Db 747 TTTTATTATTAAAGGTTAACTGGGGGCTTTTAAATTAATTTCTGTAATCTGAC 688  
Qy 1081 ATACATGGTTACACGGATATTGATCTCTGTCGTATATATCTGTTTCGAACGAGTGCC 1140  
Db 687 ATACATGGTTACACGGATATTGATCTCTGTCGTATATATCTGTTTCGAACGAGTGCC 628  
Qy 1141 GAGCCTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
Db 627 GAGCCTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 568  
Qy 1201 GTTCTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 1260  
Db 567 GTTCTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 508  
Qy 1261 GGAGTGGTAGGAGAGGGCTGGTTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320  
Db 507 GGAGTGGTAGGAGAGGGCTGGTTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 448  
Qy 1321 ATAGTGGAGGCTGTGGCTTTGTTTAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380  
Db 447 ATAGTGGAGGCTGTGGCTTTGTTTAAAGTTATCATCTAAATAACAGCACTGGAGCC 388  
Qy 1381 CACTCCCTGTCACTCCCTGGGTGATCGGGAGCAGGCCAGAAATCAACCTTTAACTTTCT 1440  
Db 387 CACTCCCTGTCACTCCCTGGGTGATCGGGAGCAGGCCAGAAATCAACCTTTAACTTTCT 328  
Qy 1441 TATTCTGTAGTATTCAAGAGGACACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 1500  
Db 327 TATTCTGTAGTATTCAAGAGGACACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 268  
Qy 1501 GTCAATTAATTAATCAATCATCATGTCCACCGCCAGAGGGCGTTCTGACTGGTTTCG 1560  
Db 267 GTCAATTAATTAATCAATCATCATGTCCACCGCCAGAGGGCGTTCTGACTGGTTTCG 208  
Qy 1561 CTGACAGTATATCCGAAGGTCGGGAGAGCGGGTGTGAAGTGCATTTTTCCTTCT 1620  
Db 207 CTGACAGTATATCCGAAGGTCGGGAGAGCGGGTGTGAAGTGCATTTTTCCTTCT 148  
Qy 1621 CCAGCGGTAAACGGTGGCGGGGTGACAGCAGCGGGGGCGGCGGAGGATCTGGCCAAAG 1680  
Db 147 CCAGCGGTAAACGGTGGCGGGGTGACAGCAGCGGGGGCGGCGGAGGATCTGGCCAAAG 88  
Qy 1681 ATGGCTGGCGGGGGCGGTGTTCTTCTTCGGTAACGCCTCTTGGATAGCTATCTGA 1740  
Db 87 ATGGCTGGCGGGGGCGGTGTTCTTCTTCGGTAACGCCTCTTGGATAGCTATCTGA 28  
Qy 1741 AAACGAAGAAGTGCCTGTAAGTATT 1767  
Db 27 AAACGAAGAAGTGCCTGTAAGTATT 1

RESULT 3  
US-10-409-613-15  
; Sequence 15, Application US/10409613  
; Publication No. US20040076635A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Phillipe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/10/409,613

; CURRENT FILING DATE: 2003-04-09  
; PRIOR FILING DATE: US/09/514,245B  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Type B PWD circovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(111)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (115)..(243)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (247)..(267)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (271)..(360)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (364)..(417)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (421)..(447)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (451)..(471)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (475)..(510)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (514)..(516)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (520)..(729)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (733)..(753)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (757)..(759)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (763)..(804)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (808)..(861)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (865)..(984)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (988)..(1173)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1177)..(1233)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1237)..(1359)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1363)..(1476)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1480)..(1737)  
; FEATURE:  
; NAME/KEY: CDS

; LOCATION: (1741)..(1767)  
US-10-409-613-15

Query Match 100.0%; Score 1767; DB 16; Length 1767;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1767: Conservative 0; Mismatches 0; Indels 0;

Qy	1	ACAGCGCACTTCGGCAGCGCGCAGCACCCTCGGCAGCAGCACCCTCAGCAGCAACATGCCCAGCA	60
Db	1	ACCAGCGCACTTCGGCAGCGCGCAGCACCCTCGGCAGCAGCACCCTCAGCAGCAACATGCCCAGCA	60
Qy	61	AGAAGATGAAGAAGCGGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTCGAATAATC	120
Db	61	AGAAGATGGAAGAACGGGACCCCAACCCCATAAAGGTGGGTGTTCACTCTCGAATAATC	120
Qy	121	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTATTGATATTTTA	180
Db	121	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTATTGATATTTTA	180
Qy	181	TTGTTGCGGAGGAGGTAATAGGAAGGACGAACACCTCACTTCAGGGGGTTCGCTAAAT	240
Db	181	TTGTTGCGGAGGAGGTAATAGGAAGGACGAACACCTCACTTCAGGGGGTTCGCTAAAT	240
Qy	241	TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCGCTGCCACATCG	300
Db	241	TTGTGAAGAAGCAGACTTTTAATAAAGTGAAGTGGTATTTGGGTGCCGCTGCCACATCG	300
Qy	301	AGAAGCGAAAGAACAGATCAGCAGAAATAAGNATATCGCAGTAAAGAGGCAACTTAC	360
Db	301	AGAAGCGAAAGAACAGATCAGCAGAAATAAGNATATCGCAGTAAAGAGGCAACTTAC	360
Qy	361	TGATCGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGGAGTGACCTGTCTACTGCTGTGA	420
Db	361	TGATCGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGGAGTGACCTGTCTACTGCTGTGA	420
Qy	421	GTA CTTGTTGGAGAGCGGGAGTCTGGTGACCGTTGCAGACGACACCCCTGTAAACGTTTG	480
Db	421	GTA CTTGTTGGAGAGCGGGAGTCTGGTGACCGTTGCAGACGACACCCCTGTAAACGTTTG	480
Qy	481	TCAGAAATTTCCCGGGCTGGCTCAA CTTTGTAAAGTGAGCGGGAAATGCAGAAAGCGTG	540
Db	481	TCAGAAATTTCCCGGGCTGGCTCAA CTTTGTAAAGTGAGCGGGAAATGCAGAAAGCGTG	540
Qy	541	ATTGGAAGACTAAATGTACACGTCAATGTGGGGCCACTGGGTGTGGTAAAGCAAATGGG	600
Db	541	ATTGGAAGACTAAATGTACACGTCAATGTGGGGCCACTGGGTGTGGTAAAGCAAATGGG	600
Qy	601	CTGCTAATTTTGACAGCCCGAAACCACTACTCGAAACCACTAGAAACAAGTGGTGGG	660
Db	601	CTGCTAATTTTGACAGCCCGAAACCACTACTCGAAACCACTAGAAACAAGTGGTGGG	660
Qy	661	ATGTTTACATGGTGAAGAGTGTGTATTTGATGACTTTATGGCTGGCTGCCCTGGG	720
Db	661	ATGTTTACATGGTGAAGAGTGTGTATTTGATGACTTTATGGCTGGCTGCCCTGGG	720
Qy	721	ATGATCTACTGAGACTGTGTGATCGATATCAATTGACTGTAGACACTAAAGGTGGAAC TG	780
Db	721	ATGATCTACTGAGACTGTGTGATCGATATCAATTGACTGTAGACACTAAAGGTGGAAC TG	780
Qy	781	TACCTTTTTTGGCCCGCAGTATCTGTATTACAGCAATCAGACCCCGTGTGGAAATGGTACT	840
Db	781	TACCTTTTTTGGCCCGCAGTATCTGTATTACAGCAATCAGACCCCGTGTGGAAATGGTACT	840
Qy	841	CCTCAACTGCTGTCCCGCTGTAGAGCTTTATCGGAGGATTA CTTCTCTGGTATTTTT	900
Db	841	CCTCAACTGCTGTCCCGCTGTAGAGCTTTATCGGAGGATTA CTTCTCTGGTATTTTT	900
Qy	901	GGAAAGTCTACAGAA CAATCCACGGAGGAAGGGGCCAGTTCGTACACCTTTCCCCCC	960
Db	901	GGAAAGTCTACAGAA CAATCCACGGAGGAAGGGGCCAGTTCGTACACCTTTCCCCCC	960
Qy	961	CATGCCCTGAATTTCCATATGAAATAAATTA CTTAGTCTTTTTTATCACTTCGTAATGGT	1020

PRECIPITATION

US-10-409-613-19/c

03-10-403-013-137 C  
: Sequence 19, Application US/10409613

: Publication No. US20040076635A1

; GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Eman

APPLICANT: Le CANN, Pie:

APPLICANT: BLANCHARD, P

; APPLICANT: HUTET, Evelyn

APPLICANT: ARNAULD, Claude

APPLICANT: TRUONG, Cath

; APPLICANT: MAHE, Dominio

; APPLICANT: CARIOLET, RO

; APPLICANT: MADEC, FRANC

; TITLE OF INVENTION: CIRCULAR DISK WITH RECORDING SURFACE OF PLASTIC MATERIAL AND METHOD OF RECORDING THEREON

; TITLE OF INVENTION: DIS  
CLOSURE REFERENCE: 065691/0

; FILE REFERENCE: 065691/0

CURRENT APPLICATION NUMBER: US/10/409,613									
CURRENT FILING DATE: 2003-04-09									
PRIOR APPLICATION NUMBER: US/09/514,245B									
PRIOR FILING DATE: 2000-02-28									
PRIOR APPLICATION NUMBER: FR 97/15396									
PRIOR FILING DATE: 1997-12-05									
NUMBER OF SEQ ID NOS: 170									
SOFTWARE: PatentIn version 3.0									
SEQ ID NO 19									
LENGTH: 1767									
TYPE: DNA									
ORGANISM: Type B PWD circovirus									
US-10-409-613-19									
Query Match 100.0%; Score 1767; DB 16; Length 1767;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ACCAGCGCACTTCGGCAGCGGAGGACCTCGGAGCACCCTCAGCAGCAACATGCCAGCA	60						
DB	1767	ACCAGCGCACTTCGGCAGCGGAGGACCTCGGAGCACCCTCAGCAGCAACATGCCAGCA	1708						
QY	61	AGAGAAATGGAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	120						
DB	1707	AGAGAAATGGAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	1648						
QY	121	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATTTT	180						
DB	1647	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATTTT	1588						
QY	181	TTGTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCACCCTCAGGGGTTCGCTAAT	240						
DB	1587	TTGTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCACCCTCAGGGGTTCGCTAAT	1528						
QY	241	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGGTGCCCGCTGCCACATCG	300						
DB	1527	TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGGTGCCCGCTGCCACATCG	1468						
QY	301	AGAAAGCGAAAGCAAGATACAGAGATTAAGAAATACCTGAGTAAAGAGGCAACTTAC	360						
DB	1467	AGAAAGCGAAAGCAAGATACAGAGATTAAGAAATACCTGAGTAAAGAGGCAACTTAC	1408						
QY	361	TGATGAGGTGGAGCTCTAGATCTCAGGGAACCGAGTGACCTGTCTACTGTGTGA	420						
DB	1407	TGATGAGGTGGAGCTCTAGATCTCAGGGAACCGAGTGACCTGTCTACTGTGTGA	1348						
QY	421	GTACCTTTGTTGGAGCGGGAGTCTGGTGAACCGTTTCAGAGCAGCAACCTGTAAAGTTG	480						
DB	1347	GTACCTTTGTTGGAGCGGGAGTCTGGTGAACCGTTTCAGAGCAGCAACCTGTAAAGTTG	1288						
QY	481	TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCAAGACGCTG	540						
DB	1287	TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCAAGACGCTG	1228						
QY	541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTAAGCAATGGG	600						
DB	1227	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTAAGCAATGGG	1168						
QY	601	CTGCTAATTTTTCAGAGCCCGGAAACCACTACTGGAACCCACCTAGAAACAGTGGTGG	660						
DB	1167	CTGCTAATTTTTCAGAGCCCGGAAACCACTACTGGAACCCACCTAGAAACAGTGGTGG	1108						
QY	661	ATGGTTACCAATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGCCCTGGG	720						
DB	1107	ATGGTTACCAATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGCCCTGGG	1048						
QY	721	ATGATCTACTCAGACTGTGTATCGATATCCATTTGACTGTAGAGCTAAAGGTGGAACTG	780						
DB	1047	ATGATCTACTCAGACTGTGTATCGATATCCATTTGACTGTAGAGCTAAAGGTGGAACTG	988						
QY	781	TACCTTTTTCGGCCCGGAGTATCTGATTTACCAGCAATCAGCCCGTTCGAATGGTACT	840						
DB	987	TACCTTTTTCGGCCCGGAGTATCTGATTTACCAGCAATCAGCCCGTTCGAATGGTACT	928						

RESULT 5  
US-10-442-180-15  
; Sequence 15, Application US/10442180  
; Publication No. US20040091502A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel

```

; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B PWD circovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(111)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (115)..(243)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (247)..(267)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)..(360)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (364)..(417)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (421)..(447)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (451)..(471)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (475)..(510)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (514)..(516)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (520)..(729)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (733)..(753)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (757)..(759)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (763)..(804)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (808)..(861)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (865)..(984)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (988)..(1173)
; FEATURE:
; NAME/KEY: CDS

```

```

; LOCATION: (1177)..(1233)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1237)..(1359)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1363)..(1476)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1480)..(1737)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1741)..(1767)
; US-10-442-180-15

Query Match      100.0%; Score 1767; DB 16; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGGCAGCGGACGACCTCGGAGCAGCCTCAGCAGCAACATGCCACGA 60
DB 1 ACCAGCGCACTTCGGCAGCGGACGACCTCGGAGCAGCCTCAGCAGCAACATGCCACGA 60
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGTGTCTCACTCTGAATAATC 120
DB 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGTGTCTCACTCTGAATAATC 120
QY 121 CTTCCGAAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTA 180
DB 121 CTTCCGAAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTA 180
QY 181 TTGTTGGCGAGGAGGGTAATGAGGAAGACGAAACACCTCACTCCAGGGGTTCCGTAATT 240
DB 181 TTGTTGGCGAGGAGGGTAATGAGGAAGACGAAACACCTCACTCCAGGGGTTCCGTAATT 240
QY 241 TTGTAAGAACGACGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
DB 241 TTGTAAGAACGACGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
QY 301 AGAAGCGAAAGGAACAGATCAGCAGAAATGAAGATATCTGCAGTAAAGAGCAACTTAC 360
DB 301 AGAAGCGAAAGGAACAGATCAGCAGAAATGAAGATATCTGCAGTAAAGAGCAACTTAC 360
QY 361 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGACAAACGAGTGACCTGTCTACTGTGTA 420
DB 361 TGATGGAGTGTGGAGCTCTTAGATCTCAGGGACAAACGAGTGACCTGTCTACTGTGTA 420
QY 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAACGTTTG 480
DB 421 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAACGTTTG 480
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCGAAGCGTG 540
DB 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCGAAGCGTG 540
QY 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600
DB 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600
QY 601 CTGCTAATTTTGCAGACCCGGAAACCAATCTGGAACCACTAGAAAACAGTGGTGGG 660
DB 601 CTGCTAATTTTGCAGACCCGGAAACCAATCTGGAACCACTAGAAAACAGTGGTGGG 660
QY 661 ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 661 ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAAC 780
DB 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAAC 780
QY 781 TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGCTACT 840
DB 781 TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGCTACT 840

```









[illegible]

Db	1501	AGTCGTC	CAATTTTAAATCTCATCTGTCACCGCCAGGAGGCGGTTGTGACTGTGGTAC	1560
Qy	1560	GCTTGCAG	TATATCCGAAGGTCGGAGAGGCGGGTGTGAAGATGCCAATTTTCCCTTC	1619
Db	1561	GCTTGCAG	TATATCCGAAGGTCGGAGAGGCGGGTGTGAAGATGCCAATTTTCCCTTC	1620
Qy	1620	TCACGCGGTAA	CGGTGGCGGGGTGACGAGCAGAGCGGGCGGCGGAGAGATCTGGCCAA	1679
Db	1621	TCCAAACGGT	TAGCGGTGGCGGGGTGACGAGCAGAGCGGGCGGCGGAGAGATCTGGCCAA	1680
Qy	1680	GATGGCTG	CGGGCGGGTGTCTTCTTCGTTAAAGCCCTCCTTGGATACGTCATATCTG	1739
Db	1681	GATGGCTG	CGGGCGGGTGTCTTCTTCGTTAAAGCCCTCCTTGGATACGTCATAGCTG	1740
Qy	1740	AAAACGAA	GAAGTGGCGCTCTAAAGTATT	1767
Db	1741	AAAACGAA	GAAGTGGCGCTCTAAAGTATT	1768
RESULT 9				
US-10-653-849-1				
; Sequence 1, Application US/10653849				
; Publication No. US20040132178A1				
; GENERAL INFORMATION:				
; APPLICANT: WANG, LI				
; APPLICANT: BABIUK, LORNE A.				
; APPLICANT: POTTER, ANDREW A.				
; APPLICANT: WILLSON, PHILIP				
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM				
; TITLE OF INVENTION: PIGS				
; FILE REFERENCE: 9000-0040				
; CURRENT APPLICATION NUMBER: US/10/653,849				
; CURRENT FILING DATE: 2003-09-02				
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/209,961				
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10				
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233				
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11				
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750				
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16				
; NUMBER OF SEQ ID NOS: 24				
; SOFTWARE: PatentIn Ver. 2.0				
; SEQ ID NO 1				
; LENGTH: 1768				
; TYPE: DNA				
; ORGANISM: Porcine Circovirus Type II				
US-10-653-849-1				
Query Match 92.2%; Score 1629.6; DB 17; Length 1768;				
Best Local Similarity 95.5%; Pred. No. 0;				
Matches 1688; Conservative 0; Mismatches 79; Indels 1; Gaps 1;				
Qy	1	ACCAGCGC	ACTTCGGCAGCGGCAGCAGCTCGGCAGCACCTCAGCAGCAACATGCCACGA	60
Db	1	ACCAGCGC	ACTTCGGCAGCGGCAGCAGCTCGGCAGCACCTCAGCAGCAACATGCCACGA	60
Qy	61	AGAAAGAT	TGGAAGAGCGGACCCCAACCCCAATAAAGGTGGTGTTCCTCTGTAATATC	120
Db	61	AGAAAGAT	TGGAAGAGCGGACCCCAACCCCAATAAAGGTGGTGTTCCTCTGTAATATC	120
Qy	121	CTTCCGAG	ACGAGCGCAGGAGAAATACGGGATCTTCCCAATCCCTATTTGATATTATTA	180
Db	121	CTTCCGAG	ACGAGCGCAGGAGAAATACGGGATCTTCCCAATCCCTATTTGATATTATTA	180
Qy	181	TTGTTGGC	GAGGGTAAATCAGGAAGGACGAAACCTCCTCCAGGGGTTCGCTAATT	240
Db	181	TTGTTGGC	GAGGGTAAATCAGGAAGGACGAAACCTCCTCCAGGGGTTCGCTAATT	240
Qy	241	TTGTGAAG	ACGACGACTTTTAAATGAAGTGGTATTTGGGTGCCCGCTGCCACATCG	300
Db	241	TTGTGAAG	ACGACGACTTTTAAATGAAGTGGTATTTGGGTGCCCGCTGCCACATCG	300
Qy	301	AGAAACGA	AGGAACAGATCAGCGAATAAAGATACTGCAGTAAAGAGGCAACTTAC	360



QY	241	TTGTGAAGAAGCAGACTTTTATAAAGTGAAGTGGTATTTGGGTGCGCGCTGCCACATCG	300
DB	241	TTGTGAAGAAGCAAACTTTTATAAAGTGAAGTGGTATTTGGGTGCGCGCTGCCACATCG	300
QY	301	AGAAAGCGAAAGGAAAGAGATCAGCAGAAATAAGATATCTGCAGTAAAGAGGCAACTTAC	360
DB	301	AGAAAGCGAAAGGAAAGTATCAGCAGAAATAAGATATTTGCAAGTAAAGAGGCAACTTAC	360
QY	361	TGATGAGGTGTGAGCTCCTAGATCTCAGGACCAACGGAGTGACCTGTCTACTGCTGTGA	420
DB	361	TTATTGAAATGTGAGCTCCTCGATCTCAAGGACCAACGGAGTGACCTGTCTACTGCTGTGA	420
QY	421	GTACCTTTGTTGGAGAGCGGAGTCTGGTGAACGTTCCAGAGCAGACCCCTGTAAAGTTTG	480
DB	421	GTACCTTTGTTGGAGAGCGGAGTCTGGTGAACGTTGCCAAAGCAGACCCCTGTAAAGTTTG	480
QY	481	TCAGAAATTTCCCGCGCTGGCTGAATCTTTGAAAGTGAGCGGAAATTCAGAGACGCTG	540
DB	481	TCAAAAATTTCCCGCGCTGGCTGAATCTTTGAAAGTGAGCGGAAATTCGAAAAGCGCTG	540
QY	541	ATTGGAAAGCTAATGTACACGTCATTTGTGGGGCCACTCGGTGTGTGTAAAGCAATGGG	600
DB	541	ATTGGAAAACCAATGTACACTTCATTTGTGGGGCCACTGGGTGTGTGTAAGCAAAATGG	600
QY	601	CTGCTAATTTTGAGACCCGGAACCACTATCTGGAAACCACTAGAAACAAGTGTGTGGG	660
DB	601	CTGCTAATTTTGCAACCCGGAACCACTATCTGGAAACCACTCTAAAAACAAGTGTGTGGG	660
QY	661	ATGGTTACCATGGTGAAGAGTGGTGTATTGATCATGACTTTTATGCTCGCTGCCCTGGG	720
DB	661	ATGGTTACCATGGTGA AAAAGTGGTGTATTGATGACTTTTATGCTCGCTGCCCTGGG	720
QY	721	ATGATCTACTGAGACTGTGTATCGATATCCATTTGACTGTAGAGACTAAAGSTGGAAC TG	780
DB	721	ATGATCTACTGAAACTGTGTATCGATATCCATTTGACTGTAAAACTAAAGSTGGAAC TG	780
QY	781	TACCTTTTGGCCGCGAGTATTTCTGATACCAAGCAATCAGACCCCGTTGGAAATGTTACT	840
DB	781	TACCTTTTGGCCGCGAGTATTTCTGATTAACCAAGCAATCAGACCCCGTTGGAAATGTTACT	840
QY	841	CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTTATCGAGAGATTACTTCTCTGGTATTTT	900
DB	841	CCTCAACTGCTGCCAGCTGTAGAAGCTCTCTATCGAGAGATTACTTCTCTGGTATTTT	900
QY	901	GGAAAGATGCTACAGAAACAATCCACGGAGGAAGGGGCCAGTTTGGTCAACCTTTCCCCC	960
DB	901	GGAAAGATGCTACAGAAACAATCCACGGAGGAAGGGGGCCAGTTTGGTCAACCTTTCCCCC	960
QY	961	CATGCCCTGAATTTCCATATGAAATAAATTTACTGAGTCTTTTTTATCAGTTCGTAATGGT	1020
DB	961	CATGCCCTGAATTTCCATATGAAATAAATTTACTGAGTCTTTTTTATCAGTTCGTAATGGT	1020
QY	1021	TTTTTATTATTCATTAAGG - TTAAGTGGGGGTCCTTTAAAAATTAATTTCTCGAAATGTA	1079
DB	1021	TTTTTATTATTCATTTAGGTTTAAGTGGGGGTCCTTTAAGATTAATTTCTCGAAATGTA	1080
QY	1080	CATACATGGTTACCGGATATTTGATTTCTGGTGTATATAC TGTTTTTGCAACGCAAGTGC	1139
DB	1081	CATACATGGTTACCGGATATTTGATGCTCGTATTTTACTGTTTTCGAAAGCAAGTGC	1140
QY	1140	CGAGGCCCTACGTGCTTACATTTCCAGCAGTTTGTAGTCTCAGGCCACAGCTGGTTCTTT	1199
DB	1141	CGAGGCCCTACGTGCTCACATTTCCAGAGGTTTGTAGCCTCAGGCCAAGCTGATTCCTTT	1200
QY	1200	TGTTGTTTGGTTGGAAGTAATCAATAGTGA AATCTAGGACAGGTTTGGGGGTAAAGTACC	1259
DB	1201	TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGGAAGTAAC	1260
QY	1260	GGGAGTGTAGGAGAGGGCTGGGTTATGTGATCGCGGAGGAGTAGTGTACATAGGGGT	1319
DB	1261	GGGAGTGTAGGAGAGGGTTGGGGGATTTGTATCGCGGAGGAGTAGTGTACATATGGGT	1320

## RESULT 11

US-10-334-245-11

US-10-334-243-11  
: Sequence 11. Application US/10334245

; sequence II, Application 05/103  
: Publication No. US20030170616A1; PUBLICATION NO: 0920  
: GENERAL INFORMATION:

APPLICANT: WANG, L.I.

APPLICANT: WANG, LI  
APPLICANT: BABIUK, IORNE A.

; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: POTTER ANDREW A.

APPLICANT: POTTER, ANDREW A.  
APPLICANT: WILSON PHILIP

APPLICANT: WILLSON, PHILIP  
TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM

TITLE OF INVENTION:
; TITLE OF INVENTION:
- TITLE OF INVENTION:

;  
; TITLE OF INVENTION: PIGS  
; REFERENCE: 8000-0040

FILE REFERENCE: 9000-0040  
CONTINUED PARTICIPATION NUMBER: IIS/1

; CURRENT APPLICATION NUMBER: US/10/334,211

; CURRENT FILING DATE: 2002-12-

; PRIOR APPLICATION NUMBER: US/09/209,961

;  
; PRIOR FILING DATE: 1998-12-10

; PRIOR APPLICATION NUMBER: 60/069,233

PRIOR FILING DATE: 1997-12-11

1. ; PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: EARLIER

NUMBER OF S

; SOFTWARE: Patco

; SEQ ID NO 11

; LENGTH: 1768

TYPE: DNA

ORGANISM: *PO*

; ORGANISM: FO  
IIS-10-334-245-11

US-TU-334-243-TT

Query Match 92.1%; Score 1628; DB 15; Length 1768;

Query Match  
Best Local Similarity 95.4%; Pred. No. 0;

BEST LOCAL SIMILARITY 55.4%;  
 Mismatches 0; Mismatches 80; Indels 1; Gaps 1;  
 Matches 1687; Conservative

MACCHER 1607; COMPETITIVE 0, INFORMATION 00)

Qy	121	CTTCCGAGACGAGCGCAAGAAATACGGATCTTCCAAATATCCCTATTGATATATTTTA	180
Db	121		
Qy	181	TTGTTGGCGAGGAGGGTAAATGAGGAAGGCGAAACACCTCACCTCCAGGGGTTTCGTAATT	240
Db	181		
Qy	241	TTGTGGAAGAAGCAGACTTTTTTAATAAGTGAAGTGGTATTGGTGCCCGCTGCCACATCG	300
Db	241		
Qy	301	AGAAAGCGAAGGAACAGATCACAGATAAAGATACTGCAGTAAAGAAGCAACTTAC	360
Db	301		
Qy	361	TGATGGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGGAGTGACCTGTCTACTGCTGTGA	420
Db	361		
Qy	421	GTACTTTGTTGGAGAGCGGAGTCTGGTGACCTTGCAGAGCAGCACCTGTAAAGTTTG	480
Db	421		
Qy	481	TCAGAAATTTCCGGCGCTGCTGAACTTTTGAAGTGAGCGGGAATAACGAGCGTG	540
Db	481		
Qy	541	ATTGGAAGACTAATGTACAGTCAATGTGGGGCCACTGGGTGTGTAAAGCAATGGG	600
Db	541		
Qy	601	CTGCTAATTTTGAGACCCGGGAACACATCTGGAACCCACCTAGAAAACAAGTGTGGG	660
Db	601		
Qy	661	ATGGTTACCATGGTGAAGAAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
Db	661		
Qy	721	ATGATCTACTGAGACTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAACTG	780
Db	721		
Qy	781	TACCTTTTTTGGCCCGCAGTATCTGATTACCAAGCAATCAGACCCGTTGGAATGGTACT	840
Db	781		
Qy	841	CCTCAACTGCTGTCGCCAGCTGTAGAAGCTTTATCGAGGATTACTTCCTTGGTATTTT	900
Db	841		
Qy	901	GGAGAAATGCTACAGAAACAATCCAGGAGGAAGGGGGCAGTTCGTACCCCTTCCCCCC	960
Db	901		
Qy	961	CATGCCCTGAATTTCCATATGAATAAATACTGAGTCTTTTTTATCACTTCGTAATGGT	1020
Db	961		
Qy	1021	TTTTATTATTCATTAAGGG- TTAAGTGGGGGTCCTTTAAAAATTAATTCCTGAAATGTGA	1079
Db	1021		
Qy	1080	CATACATGGTTACACGGATAATTGTATTCTTGGTCGTATATACTGTTTTTCGAACCGAGTGC	1139
Db	1081		
Qy	1140	CGAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGGCCACAGCTGGTTCTTTT	1199
Db	1141		
Qy	1200	TGTTGTTTGGTGGAAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC	1259

1201	DB		TGTTATTTGGTTGGAAAGTAAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGCAAGTAAC	1260
1260	QY		GGCAGTGTAGGAGAAAGGGCTGGGTTTATGTTATGGCGGAGGAGTAGTTTACATAGGGGT	1319
1261	DB		GGAGTGTAGGAGAAAGGGTGGGGGATTTGTATGGCGGAGGAGTAGTTTACATATGGGT	1320
1320	QY		CATAGGTGAGGGCTGTGGCCCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGC	1379
1321	DB		CATAGGTTAGGGCTGTGGCCCTTTGTTTACAAAGTTATCATCTAAATAACAGCAGTGGAGC	1380
1380	QY		CCACTCCCTGTCCACCTGGGTGATCGGGAGCAGGGCCAGAAATTCACACTTAAACCTTTC	1439
1381	DB		CCACTCCCTTATCACCTGGGTGATCGGGGAGCAGGGCCAGAAATTCACACTTAAACCTTTC	1440
1440	QY		TTATTCTGTAGTATTCAAAGGGCACAGCGGGGGTTGACCCCTCTCTGGGGGAAGAA	1499
1441	DB		TTATTCTGTAGTATTCAAAGGGTATAGAGATTTTGTGTGCCCTCTCCGGGGGAACAA	1500
1500	QY		AGTCATTTAAATTTGAATCTCATCATGTCCACGCCCCAGAGGGCGTTCTGACCTGTGGTTC	1559
1501	DB		AGTCGTCAATTTTAAATCTCATCATGTCCACGCCCCAGAGGGCGTTGTCACCTGTGGTAC	1560
1560	QY		GCITTCACAGATATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTTCCTTC	1619
1561	DB		GCITTCACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTTCCTTC	1620
1620	QY		TCCAGCGGTTAACGTTGCGGGGGTGGACGAGCCAGAGGGCGCGCGAGGATCTGGCCAA	1679
1621	DB		TCCAACGGTATGCGGTGCGGGGGTGGACGAGCCAGAGGGCGCGCGAGGAGTCTGGCCAA	1680
1680	QY		GATGGCTGCGGGGGCGGTGTCTTCTTCTTCGGTAAACGCCCTCTTGGGATACGTCATATCTG	1739
1691	DB		GATGGCTGCGGGGGCGGTGTCTTCTTCTTCGGTAAACGCCCTCTTGGGATACGTCATAGCTG	1740
1740	QY		AAAAACGAAAGTGTGCGGTGTAGTATT	1767
1741	DB		AAAAACGAAAGTGTGCGGTGTAGTATT	1768

## RESULT 12

RES001 12  
US-10-653-849-11  
; Sequence 11, Application US/10653849  
; Publication No. US20040132178A1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, LI  
; APPLICANT: BABIUK, LORNE A.  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: WILLSON, PHILIP  
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM  
; TITLE OF INVENTION: PIGS  
; FILE REFERENCE: 9000-0040  
; CURRENT APPLICATION NUMBER: US/10/653,849  
; CURRENT FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/209,961  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,750  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-16  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine Circovirus Type II  
US-10-653-849-11

Query Match 92.1%; Score 1628; DB 17; Length 1768;  
Best Local Similarity 95.4%; Pred. No. 0;  
Matches 1687; Conservative 0; Mismatches 80; Indels 1; Gaps 1  
QY 1 ACCAGCGCACTTGGCGACGGCGAGCACTTCGGCAGCAGCTCAGCAGCAACATGCCACGA 60

```

1  ACCAGCGCACTTCGCGAGCGGAGCACCTCGCGAGCACCTCAGCAGCAACATGCCAGCA 60
61  AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGTAATATC 120
61  AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGTAATATC 120
121  CTTCCGAAGACGAGCGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTTAA 180
121  CTTCCGAAGACGAGCGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTTAA 180
181  TTGTTGGCGAGGAGGTTAATGAGGAAGCAACCTCAGGAGTTCGTAATTT 240
181  TTGTTGGCGAGGAGGTTAATGAGGAAGCAACCTCAGGAGTTCGTAATTT 240
241  TTGTTGAAGCAAGCACTTTTAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
241  TTGTTGAAGCAAGCACTTTTAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
301  AGAAGCGAAAGGACAGATCAGCAGATAAAGATACTGCAGTAAAGAGGCAACTTAC 360
301  AGAAGCGCAAGGAACTGATCAGCAGATAAAGATACTGCAGTAAAGAGGCAACTTAC 360
361  TGATGAGTGTGAGCTCCTAGATCTCAGGAGCAACCGAGTGAACCTGTCTACTGTGTA 420
361  TTATTTGAATGTGAGCTCCTAGATCTCAGGAGCAACCGAGTGAACCTGTCTACTGTGTA 420
421  GTACCTTTGTTGAGAGCGGGATTCCTGAGCGCTTGAAGAGCAGCACCTGTAAAGTTG 480
421  GTACCTTTGTTGAGAGCGGGATTCCTGAGCGCTTGAAGAGCAGCACCTGTAAAGTTG 480
481  TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCAGAAAGCGTG 540
481  TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAATGCAGAAAGCGTG 540
541  ATTGGAAGACTAATGTACACGTCTATTTGGGCGCCACCTGGGTGGTAAAGCAATGGG 600
541  ATTGGAAGACTAATGTACACGTCTATTTGGGCGCCACCTGGGTGGTAAAGCAATGGG 600
601  CTGCTAATTTTGCAGACCGGAAACCAATATCTGAAACCACTAAGAGTGGTGGG 660
601  CTGCTAATTTTGCAGACCGGAAACCAATATCTGAAACCACTAAGAGTGGTGGG 660
661  ATGGTTACCATGCTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
661  ATGGTTACCATGCTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
721  ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGTGGAACTG 780
721  ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGTGGAACTG 780
781  TACCTTTTGGCGCGAGTATTCGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
781  TACCTTTTGGCGCGAGTATTCGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
841  CCTCAACTGCTGCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
841  CCTCAACTGCTGCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900
901  GGAAGAAATGCTACAGAAACCAATCCACCGAGGAGGCGGCGAGTTCGTACCCCTTTCCGCC 960
901  GGAAGAAATGCTACAGAAACCAATCCACCGAGGAGGCGGCGAGTTCGTACCCCTTTCCGCC 960
961  CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTATCATTGTAATGGT 1020
961  CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTATCATTGTAATGGT 1020
1021  TTTTATTTATCATTAAGG-TTAAGTGGGGCTTTTAAATTAATTTCTGAAATGTA 1079
1021  TTTTATTTATCATTTAAGGTTAAGTGGGGCTTTTAAATTAATTTCTGAAATGTA 1080
1080  CATACATGGTTACCGGATTTGATTTCTTGGTGGTATATCTGTTTTCGAAAGCAGTGC 1139

```

```

1081  CATACATGGTTACAGGATATTGTAGTCTCGTATTTACTGTTTTCGAACGAGTGC 1140
1140  CGAGCCCTAGTGGTCTACATTTTCCAGCAGTTTGTAGTCTCAGCACAGCTGGTTCTTT 1199
1141  CGAGCCCTAGTGGTCTACATTTTCCAGAGGTTTGTAGCTCAGCCAAAGCTGATTCCTTT 1200
1200  TGTGTTTGGTTGGAAGTAACTCAATAGTGAATCTAGACAGGTTTGGGGTGAAGTACC 1259
1201  TGTATTTGGTTGGAAGTAACTCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAA 1260
1260  GGGAGTGTAGCAGAGGGCTGGGTATGGTATGGCGGAGGAGTAGTTTACATAGGGGT 1319
1261  GGGAGTGTAGCAGAGGGTTGGGGATTTGATGGCGGAGGAGTAGTTTACATATGGGT 1320
1320  CATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCAGTGGAGC 1379
1321  CATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCAGTGGAGC 1380
1380  CCATCCCTGTACCTCGGTGATCGGGAGCAGGGCCAGAAATTCACCTTAACTTTC 1439
1381  CCATCCCTGTACCTCGGTGATGGGGAGCAGGGCCAGAAATTCACCTTAACTTTC 1440
1440  TTATTTCTAGTATTTCAAGGGCACAGAGCGGGGTTTGACCCCTCTCGGGGAGAA 1499
1441  TTATTTCTAGTATTTCAAGGGTATAGAGATTTTGTGGTCCCTCCCGGGGAGCAA 1500
1500  AGTCATTAATTTGAATCTCATGTCCACCGCCAGAGGGGCTTCTGACTGTGGTTC 1559
1501  AGTCATTAATTTGAATCTCATGTCCACCGCCAGAGGGGCTTCTGACTGTGGTTC 1560
1560  GCTTGACAGTATATCCGAAGTGGGGAGAGCGGGTGTGAGAGTGCATTTTCTTC 1619
1561  GCTTGACAGTATATCCGAAGTGGGGAGAGCGGGTGTGAGAGTGCATTTTCTTC 1620
1620  TCCAGCGGTAAACGTTGGCGGGTGGAGCGAGCGGGCGGGCGGAGGATCTGGCCAA 1679
1621  TCCAGCGGTAGCGTTGGCGGGTGGAGCGAGCGGGCGGGCGGAGGATCTGGCCAA 1680
1680  GATGCTCGGGGGCGGTGTCTTCTTCGCTAAGCGCTCTCTGATACGTATAGCTG 1739
1681  GATGCTCGGGGGCGGTGTCTTCTTCGCTAAGCGCTCTCTGATACGTATAGCTG 1740
1740  AAAACGAAAGATGCGCTGTAAATTT 1767
1741  AAAACGAAAGATGCGCTGTAAATTT 1768

```

```

RESULT 13
US-10-112-540-1
; Sequence 1, Application US/10112540
; Publication No. US20020177216A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; APPLICANT: Tikoo, Suresh K.
; APPLICANT: Willson, Philip
; APPLICANT: Babiuk, Lorne A.
; TITLE OF INVENTION: METHODS TO CULTURE CIRCOVIRUS
; FILE REFERENCE: 293102003100
; CURRENT APPLICATION NUMBER: US/10/112,540
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/279,173
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-10-112-540-1

```

```

Query Match          91.7%; Score 1620; DB 13; Length 1768;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 1682; Conservative 0; Mismatches 85; Indels 1; Gaps 1;

```



QY 1 ACCAGCGACCTTCGGCAGCGCAGCACCTCGGCAGCACCTCAGCAGCAAAATGCCCCAGCA 60  
Db 1 ACCAGCGACCTTCGGCAGCGCAGCACCTCGGCAGCACCTCAGCAGCAAAATGCCCCAGCA 60  
QY 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATATC 120  
Db 61 AGAAGAAATGGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATATC 120  
QY 121 CTTCCGAAGACGAGGCGAAGAAATACGGGATCTCCAAATCTCCCTATTTGATTTATTTA 180  
Db 121 CTTCCGAAGACGAGGCGAAGAAATACGGGATCTCCAAATCTCCCTATTTGATTTATTTA 180  
QY 181 TTGTTGGCGAGGAGTAAATCAGGAAGACCAACACCTCACCTCAGGGGTTCGCTAAT 240  
Db 181 TTGTTGGCGAGGAGTAAATCAGGAAGACCAACACCTCACCTCAGGGGTTCGCTAAT 240  
QY 241 TTGTGAAGACGACACTTTTAAATGAAGTGAAGTGAATTTGGGTGCCCGCTGCCACATCG 300  
Db 241 TTGTGAAGACGACACTTTTAAATGAAGTGAAGTGAATTTGGGTGCCCGCTGCCACATCG 300  
QY 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGATCTCAGTAAGAGGCAACTTAC 360  
Db 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGATCTCAGTAAGAGGCAACTTAC 360  
QY 361 TGATGGAGTGGAGCTCCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGCTGTA 420  
Db 361 TTATTGAATGTGAGCTCTCGATCTCAAGACCAACGAGTGACCTGTCTACTGCTGTA 420  
QY 421 GTACCTTGTGGAGAGCGGAGTCTGGTGAACGTTGACAGAGCAGCACCTGTAAAGTTG 480  
Db 421 GTACCTTGTGGAGAGCGGAGTCTGGTGAACGTTGACAGAGCAGCACCTGTAAAGTTG 480  
QY 481 TCAGAAATTCGCGGGTGGCTGAACCTTTGAAAGTGAAGGAGGAAATCAGAGCGTG 540  
Db 481 TCAGAAATTCGCGGGTGGCTGAACCTTTGAAAGTGAAGGAGGAAATCAGAGCGTG 540  
QY 541 ATTGAAGACTAATCTACACGCTCATTTGTGGGCGCACCTGGGTGGTAAAGCAAAATGGG 600  
Db 541 ATTGAAGACTAATCTACACGCTCATTTGTGGGCGCACCTGGGTGGTAAAGCAAAATGGG 600  
QY 601 CTGCTAAATTTGACAGACCGGAAACCAATATCGAAACCACTAGAAACAAAGTGGTGG 660  
Db 601 CTGCTAAATTTGACAGACCGGAAACCAATATCGAAACCACTAGAAACAAAGTGGTGG 660  
QY 661 ATGGTTACCATGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGG 720  
Db 661 ATGGTTACCATGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGG 720  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCAGCTGAGACTAAAGGTGAACTG 780  
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTCAGCTGAGACTAAAGGTGAACTG 780  
QY 781 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCGCTTGGAAATGGTACT 840  
Db 781 TACCTTTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCGCTTGGAAATGGTACT 840  
QY 841 CCTCAACTGCTCTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900  
Db 841 CCTCAACTGCTCTCCAGCTGTAGAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900  
QY 901 GGAAGAACTCTACAGAAACATCCAGGAGGAGGCGGCGAGTTCGTCACCTTTCCCCC 960  
Db 901 GGAAGAACTCTACAGAAACATCCAGGAGGAGGCGGCGAGTTCGTCACCTTTCCCCC 960  
QY 961 CATGCCCTGAATTCATATGAATAAATATCTAGTCTTTTATCACTTCGTAATGGT 1020  
Db 961 CATGCCCTGAATTCATATGAATAAATATCTAGTCTTTTATCACTTCGTAATGGT 1020  
QY 1021 TTTTATTATTCATTAGGG-TTAAAGTGGGGGTCTTTAAATTAATCTCTGAATTTGA 1079  
Db 1021 TTTTATTATTCATTAGGGTTAAAGTGGGGGTCTTTAAAGTAAATCTCTGAATTTGA 1080

QY 1080 CATACATGTTACACGGATATTGATTTCTCTGTCGTATATCTGTTTTCGAACGCAGTGC 1139  
Db 1081 CATACATGTTACACGGATATTGATTTCTCTGTCGTATATCTGTTTTCGAACGCAGTGC 1140  
QY 1140 CGAGGCTACGTCGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT 1199  
Db 1141 CGAGGCTACGTCGTCCACATTTCTAGAGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT 1200  
QY 1200 TGTGTTTGTGTTGCGAAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC 1259  
Db 1201 TGTATTTGTGTTGGAAGTAAATCAATAGTGAATCAAGAACAGGTTTGGGTGTGAAGTAA 1260  
QY 1260 GGAGTGTAGGAGAGGCTGGGTATAGTATGGCGGAGGAGTAGTTTACATAGGGGT 1319  
Db 1261 GGAGTGTAGGAGAGGCTGGGGATTTGATGGCGGAGGAGTAGTTTACATATGGGT 1320  
QY 1320 CATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGC 1379  
Db 1321 CATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGC 1380  
QY 1380 CCACTCCCTGTGTCACTGGGTGATCGGGAGCAGGCGCCAGAAATTCACCTTAACTTTTC 1439  
Db 1381 CCACTCCCTGTGTCACTGGGTGATCGGGAGCAGGCGCCAGAAATTCACCTTAACTTTTC 1440  
QY 1440 TTATTTGTAGTATTCAAAGGACAGAGCGGGGTTTGACCCCTCTCTGGGGGAGAA 1499  
Db 1441 TTATTTGTAGTATTCAAAGGCTATAGAGATTTTGTGGTCCCCCTCCCGGGGAAACAA 1500  
QY 1500 AGTCAATTAATTAATCTCATCTCATCTGTCACCGCCAGGAGGCGTTCTGACCTGTGGTTC 1559  
Db 1501 AGTGTCAATTAATTAATCTCATCTCATCTGTCACCGCCAGGAGGCGTTCTGACCTGTGGTAG 1560  
QY 1560 GCTTGACAGTATATCCGAAGGTGCGGAGAGGCGGTGTTGAAGATGCCATTTTCTCTTC 1619  
Db 1561 CCTTGACAGTATATCCGAAGGTGCGGAGAGGCGGTGTTGAAGATGCCATTTTCTCTTC 1620  
QY 1620 TCCAGCGGTAAAGTGGCGGGGTGGAGCAGCAGCGCGCGCGGAGGATCTGGCCAA 1679  
Db 1621 TCCAAAGGTAAAGTGGCGGGGTGGAGCAGCAGCGCGCGCGGAGGATCTGGCCAA 1680  
QY 1680 GATGCTGCGGGCGGTGCTCTCTCTCGTAAACCCCTCTTGGATAGCTCATATCTG 1739  
Db 1681 GATGCTGCGGGCGGTGCTCTCTCTCGTAAACCCCTCTTGGATAGCTCATATCTG 1740  
QY 1740 AAAACGAAAGAGTGCCTGTAAAGTATT 1767  
Db 1741 AAAACGAAAGAGTGCCTGTAAAGTATT 1768

## RESULT 14

US-09-784-962-1  
; Sequence 1, Application US/09784962  
; Patent No. US20020146431A1  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/784,962  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: 09/347,594  
; PRIOR FILING DATE: 1999-07-04  
; PRIOR APPLICATION NUMBER: 98 08777  
; PRIOR FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus



US-09-784-962-1

```
Query Match          79.9%; Score 1412; DB 9; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGCGAGCGGAGCACTCGCGAGCACCTCGCGAGCACCTCGAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGCGAGCGGAGCACTCGCGAGCACCTCGAGCAACATGCCAGCA 407

QY 61 AGAAGATGGAAGACGGAACCCCAACCCCATAAAGGTGGGTCTCACTGTAATATC 120
DB 408 AGAAGATGGAAGACGGAACCCCAACCCCATAAAGGTGGGTCTCACTGTAATATC 467

QY 121 CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATATTTA 180
DB 468 CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATATTTA 527

QY 181 TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAAT 240
DB 528 TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAAT 587

QY 241 TTGTAAGACGAGCACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 300
DB 588 TTGTAAGACGAGCACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 647

QY 301 AGAAGCGAAGGACGATCAGCAGATTAAGAAATACCTGCACTGAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGGACGATCAGCAGATTAAGAAATACCTGCACTGAAGAGGCAACTTAC 707

QY 361 TCATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTGAACCTGTCTACTGTGTA 420
DB 708 TCATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTGAACCTGTCTACTGTGTA 767

QY 421 GTACCTTGTGAGAGCGGAGTGTGTGACCGCTGTCAGAGCAGACCCCTGTAAAGTTG 480
DB 768 GTACCTTGTGAGAGCGGAGTGTGTGACCGCTGTCAGAGCAGACCCCTGTAAAGTTG 827

QY 481 TCAGAAATTTCCGCGGCTGGCTGACCTTTTCAAGTGAAGGGAATGCAAGACGCTG 540
DB 828 TCAGAAATTTCCGCGGCTGGCTGACCTTTTCAAGTGAAGGGAATGCAAGACGCTG 887

QY 541 ATTGGAAGACTAATGTACACGCTCATTTGGGGCCACTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACACGCTCATTTGGGGCCACTGGGTGTGTTAAAGCAATGGG 947

QY 601 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACACCTAGAAACAAGTGTGGG 660
DB 948 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACACCTAGAAACAAGTGTGGG 1007

QY 661 ATGGTTACCATGTTGAAGAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGGTTACCATGTTGAAGAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGG 1067

QY 721 ATGATCTACTGACACTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 780
DB 1068 ATGATCTACTGACACTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTGGAAATGTACT 840
DB 1128 TACCTTTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTGGAAATGTACT 1187

QY 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 1247

QY 901 GGAAGATGCTACAGAACCAATCCACGAGGAAGCGGCGAGTTTCCTCACCTTTCCCGCC 960
DB 1248 GGAAGATGCTACAGAACCAATCCACGAGGAAGCGGCGAGTTTCCTCACCTTTCCCGCC 1307

QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGTT 1020
DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGTT 1367
```

```
QY 1021 TTTTATTATTATTAAGGTTAACTGGGGGTCTTTTAAATTAATTAATCTCTGAATTGTAC 1080
DB 1368 TTTTATTATTATTAAGGTTAACTGGGGGTCTTTTAAAGATTAAATTTCTCTGAATTGTAC 1427

QY 1081 ATACATGGTTACACGGATATTTGTTATCTCTGGTCCGTATATCTGTTTTCGAACGAGTGCC 1140
DB 1428 ATACATGGTTACACGGATATTTGTTATCTCTGGTCCGTATATCTGTTTTCGAACGAGTGCC 1487

QY 1141 GAGCCCTACGTTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACACAGCTGTTCTTTT 1200
DB 1488 GAGCCCTACGTTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACACAGCTGTTCTTTT 1547

QY 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607

QY 1261 GGAGTGTAGGAGAGGCTGGGTTATGGTATGGGAGGAGTAGTTTTACATAGGGGTC 1320
DB 1608 GGAGTGTAGGAGAGGCTGGGTTATGGTATGGGAGGAGTAGTTTTACATAGGGGTC 1667

QY 1321 ATAGTGAGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATAAACAGCACTGAGGCC 1380
DB 1668 ATAGTGAGGCTGTGGCTTTTGTACAAAGTTATCATCTAGATAAACAGCACTGAGGCC 1727

QY 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1767

RESULT 15
US-09-884-514-1
; Sequence 1, Application US/09884514
; Patent No. US20020146432A1
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREIRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-1

Query Match          79.9%; Score 1412; DB 9; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGCGCACTTCGCGAGCGGAGCACTCGCGAGCACCTCGCGAGCACCTCGAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGCGAGCGGAGCACTCGCGAGCACCTCGAGCAACATGCCAGCA 407

QY 61 AGAAGATGGAAGACGGAACCCCAACCCCATAAAGGTGGGTCTCACTGTAATATC 120
DB 408 AGAAGATGGAAGACGGAACCCCAACCCCATAAAGGTGGGTCTCACTGTAATATC 467

QY 121 CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATATTTA 180
DB 468 CTTCCGAGACGAGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTGTAATATTTA 527

QY 181 TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAAT 240
DB 528 TTGTTGGCGAGGAGGTAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGTAAT 587

QY 241 TTGTAAGACGAGCACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 300
DB 588 TTGTAAGACGAGCACTTTTAATAAGTGAAGTGTATTTGGGTCCCGCTGCCACATCG 647

QY 301 AGAAGCGAAGGACGATCAGCAGATTAAGAAATACCTGCACTGAAGAGGCAACTTAC 360
DB 648 AGAAGCGAAGGACGATCAGCAGATTAAGAAATACCTGCACTGAAGAGGCAACTTAC 707

QY 361 TCATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTGAACCTGTCTACTGTGTA 420
DB 708 TCATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTGAACCTGTCTACTGTGTA 767

QY 421 GTACCTTGTGAGAGCGGAGTGTGTGACCGCTGTCAGAGCAGACCCCTGTAAAGTTG 480
DB 768 GTACCTTGTGAGAGCGGAGTGTGTGACCGCTGTCAGAGCAGACCCCTGTAAAGTTG 827

QY 481 TCAGAAATTTCCGCGGCTGGCTGACCTTTTCAAGTGAAGGGAATGCAAGACGCTG 540
DB 828 TCAGAAATTTCCGCGGCTGGCTGACCTTTTCAAGTGAAGGGAATGCAAGACGCTG 887

QY 541 ATTGGAAGACTAATGTACACGCTCATTTGGGGCCACTGGGTGTGTTAAAGCAATGGG 600
DB 888 ATTGGAAGACTAATGTACACGCTCATTTGGGGCCACTGGGTGTGTTAAAGCAATGGG 947

QY 601 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACACCTAGAAACAAGTGTGGG 660
DB 948 CTGCTAATTTTCAGACCCGGAACACATATCTGGAACACCTAGAAACAAGTGTGGG 1007

QY 661 ATGGTTACCATGTTGAAGAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1008 ATGGTTACCATGTTGAAGAGTGGTTGTTATTGATGACTTTTATGGCTGGCTGCCCTGG 1067

QY 721 ATGATCTACTGACACTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 780
DB 1068 ATGATCTACTGACACTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTGGAAATGTACT 840
DB 1128 TACCTTTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTGGAAATGTACT 1187

QY 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTACTTCTTGGTATTTT 1247

QY 901 GGAAGATGCTACAGAACCAATCCACGAGGAAGCGGCGAGTTTCCTCACCTTTCCCGCC 960
DB 1248 GGAAGATGCTACAGAACCAATCCACGAGGAAGCGGCGAGTTTCCTCACCTTTCCCGCC 1307

QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGTT 1020
DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGTT 1367
```

Db 408 AGAAGATGGAAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGATTAATC 467  
Qy 121 CTTCCGAAGACGACGCGCAAGAAAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180  
Db 468 CTTCCGAAGACGACGCGCAAGAAAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 527  
Qy 181 TTGTTGGCGAGGAGGTAAATGAGAGGACGAACACCTCACCTCCAGGGGTTCGCTAAAT 240  
Db 528 TTGTTGGCGAGGAGGTAAATGAGAGGACGAACACCTCACCTCCAGGGGTTCGCTAAAT 587  
Qy 241 TTGTTGAGAACGACAGCTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300  
Db 588 TTGTTGAGAACGACAGCTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647  
Qy 301 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 360  
Db 648 AGAAGCGAAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 707  
Qy 361 TGATGGAGTGGAGCTCCTAGATCTCAGGACACAGGAGTGAACCTGTCTACTCTGTGA 420  
Db 708 TGATGGAGTGGAGCTCCTAGATCTCAGGACACAGGAGTGAACCTGTCTACTCTGTGA 767  
Qy 421 GTACCTCTGTGGAGACGGGAGTCTGTGACCGTTGCAGAGCAGCACCTGTAACTGTTG 480  
Db 768 GTACCTCTGTGGAGACGGGAGTCTGTGACCGTTGCAGAGCAGCACCTGTAACTGTTG 827  
Qy 481 TCAGAAATTTCCGCGGGTGGCTGAATTTTGAAGTGAAGCGGGAATGAGAGCGTG 540  
Db 828 TCAGAAATTTCCGCGGGTGGCTGAATTTTGAAGTGAAGCGGGAATGAGAGCGTG 887  
Qy 541 ATTGAAGACTAATGTACACGTCATTTGTGGGCCACCTGGGTGTGTAAGAAAGCAATGGG 600  
Db 888 ATTGAAGACTAATGTACACGTCATTTGTGGGCCACCTGGGTGTGTAAGAAAGCAATGGG 947  
Qy 601 CTGCTAAATTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660  
Db 948 CTGCTAAATTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 1007  
Qy 661 ATGGTTACATGGTGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720  
Db 1008 ATGGTTACATGGTGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
Qy 721 ATGATCTACTGACACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAACCTG 780  
Db 1068 ATGATCTACTGACACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAAGGTGGAACCTG 1127  
Qy 781 TACCTTTTGGCCCGCAGTATTTCTGAATACCAAGCAATCAGACCCCGTTGGAATGGTACT 840  
Db 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 1187  
Qy 841 CCTCAACTGTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 900  
Db 1188 CCTCAACTGTGTCCAGCTGTAGAAGCTTTTATCGGAGGATTAATCTCTTGGTATTTT 1247  
Qy 901 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCAACCTTTCCCCCC 960  
Db 1248 GGAAGATGCTACAGAACCAATCCACGAGGAGGCGGCGAGTTTCGTCAACCTTTCCCCCC 1307  
Qy 961 CATGCCCTGAATTTCCATATGAATAAATPACTGAGTCTTTTTTATCACTTCGTAATGGT 1020  
Db 1308 CATGCCCTGAATTTCCATATGAATAAATPACTGAGTCTTTTTTATCACTTCGTAATGGT 1367  
Qy 1021 TTTTATTTATTAAGGGTTAAGTGGGGTCTTTTAAATTAATTAATTTCTGTAATTTGATAC 1080  
Db 1368 TTTTATTTATTAAGGGTTAAGTGGGGTCTTTTAAAGATTAAATTTCTGTAATTTGATAC 1427  
Qy 1081 ATACATGTTTACAGGATATTTGATTTCTGCTGTATATATCTGTTTTCGAACGAGTGCC 1140  
Db 1428 ATACATGTTTACAGGATATTTGATTTCTGCTGTATATATCTGTTTTCGAACGAGTGCC 1487  
Qy 1141 GAGGCTTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200  
Db 1488 GAGGCTTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1547

Qy 1201 GTTGTGTTGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260  
Db 1548 GTTGTGTTGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGTAAAGTACCG 1607  
Qy 1261 GGAGTGGTAGGAGAAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1320  
Db 1608 GGAGTGGTAGGAGAAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1667  
Qy 1321 ATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380  
Db 1668 ATAGGTGAGGGCTGTGGCCTTTGTTACAAAGTTATCATCTAGAAATAACAGCACTGGAGCC 1727  
Qy 1381 CACTCCCTGTGTCAACCTGGGTGATCGGGAGCAGGGCCAG 1420  
Db 1728 CACTCCCTGTGTCAACCTGGGTGATCGGGAGCAGGGCCAG 1767

Search completed: December 8, 2004, 00:59:58  
Job time : 934 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:40:50 ; Search time 5729 Seconds  
(without alignments)  
11239.135 Million cell updates/sec

Title: US-10-718-264-15

Perfect score: 1767  
Sequence: 1 accagcgcaactcgagcgcg.....agaagtgcgtgaagtatt 1767

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsal:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48.2	2.7	1101	CNS00LT2	AL078714 Drosophil
2	47.8	2.7	1101	CNS00L00	AL068607 Drosophil
3	46.6	2.6	661	CA297536	SCCSD1C0
4	46.6	2.6	922	CNS0073W	AL066784 Drosophil
5	45.6	2.6	497	CA294389	SCSGLV101
6	45.6	2.6	598	CA294459	SCSGLV101
7	45.6	2.6	667	CA108913	SCSGHR106
8	45.4	2.6	561	AL1514058	AL1514058 GH27112.5
9	45.2	2.6	324	CE373054	tigr-gss-
10	45.2	2.6	1029	AG034053	Pan trogl
11	45	2.5	571	CA741621	wiaic.pk0
12	45	2.5	603	CA103262	SCZHR104
13	45	2.5	622	CA300454	SCSFLV104
14	45	2.5	640	CA198894	SCSGFL107
15	45	2.5	721	CA104948	SCUFR1C0
16	45	2.5	1043	CA278752	SCCSD209
17	44.8	2.5	560	CA222795	SCZFLA03
18	44.8	2.5	818	AZ175609	SP_0132_A
19	44.6	2.5	756	6	CA066540
20	44.6	2.5	939	CNS00CNG	AL055400 Drosophil
21	44.2	2.5	638	4	BI629442 RH58310.5
22	44.2	2.5	946	6	CA103549 SCEZHR108
23	44	2.5	331	5	BU064153 Fgr_4_B22
24	44	2.5	389	5	BU065797 Fgr_8_I14

25	44	2.5	400	5	BU064605
26	44	2.5	431	5	BU060128
27	44	2.5	445	1	AI292664
28	44	2.5	463	5	BU061818
29	44	2.5	474	5	BU060441
30	44	2.5	483	5	BU063808
31	44	2.5	483	5	BU063868
32	44	2.5	484	1	AI108264
33	44	2.5	489	5	BU063869
34	44	2.5	492	5	BU060442
35	44	2.5	493	1	AI405757
36	44	2.5	497	1	AI238309
37	44	2.5	504	5	BU059468
38	44	2.5	520	5	BU063809
39	44	2.5	532	1	AI134557
40	44	2.5	535	5	BU059427
41	44	2.5	535	5	BU061852
42	44	2.5	551	5	BU060660
43	44	2.5	557	1	AI404106
44	44	2.5	557	1	AI406114
45	44	2.5	558	1	AI238565

#### ALIGNMENTS

RESULT 1  
CNS00LT2 1101 bp DNA linear GSS 14-JUN-1999  
Drosophila melanogaster genome survey sequence TET3 end of BAC:  
BAC48P19 of RPI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL078714.1 GI:5102004

KEYWORDS GSS.  
Drosophila melanogaster (fruit fly)

SOURCE Drosophila melanogaster

ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

AUTHORS

TITLE

JOURNAL

COMMENT

Genoscope - Centre National de Sequencage :  
Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pister de Jong's laboratory at the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pi and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
Location/Qualifiers  
1..1101  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BAC48P19"  
/clone\_lib="RPI-98"  
/note="end : TET3"

ORIGIN

Query Match 2.7%; Score 48.2; DB 9; Length 1101;  
Best Local Similarity 19.3%; Pred. No. 0.039;

Matches	73;	Conservative	139;	Mismatches	167;	Indels	0;	Gaps	0;			
Qy	972	TTTCCATATGA	AAATAAATTAC	GAGTC	TTTTTTATC	ACATTCGTA	ATGGTTTTT	TATTATTC	1031			
Db	629	TTTAAATTTT	TTTWTAWATTT	TTTTTTTAK	TTTTTTTTTTT	TATTA	AAAAAAWT	688				
Qy	1032	ATTAAGGGT	TAAAGTGGGGG	CTTTAAAT	TAAATCTCT	GAATTCG	TACATACAT	CGTTA	1091			
Db	689	TDTAAAW	TTTTTTTTTTTT	KKKKKAA	AAADKKW	DAKKATTT	KKDKKAA	AAADKKDKK	748			
Qy	1092	CACGATAT	TGTTATCT	CGTCGTAT	ATATCTG	TTTTCGA	ACGACGAGT	CCGAGCC	TACGT	1151		
Db	749	GKKKGK	KGKGGKKKK	KKKKGGK	GKGGK	KKKAGD	DAKDKT	KKKKKCA	TTTTTKKK	808		
Qy	1152	GGTCTAC	ATTTTC	CAGCAGT	TTTGTAG	CTC	CAGCCAC	CAGCTGG	TTTTTCTTTT	TGTTGGTT	1211	
Db	809	GKKKKK	AAKKKAA	ADRTK	TKWD	AAAAAA	AAAKK	TKDKG	KKKKTK	TKTTTKKKKKKKKK	868	
Qy	1212	GGAAGT	TAATCA	ATAGTGA	AAATCTAG	GACAG	GGTTTGGGG	GTTAA	AGTACCG	GAGATGGT	TAGG	1271
Db	869	GGGKK	DAAAKKK	KKGT	KKKKG	KGKGG	KGKGG	KKKDD	DAAAKKK	GGKKKKGGGG	928	
Qy	1272	AGAAGGG	CTGGTTAT	TGTTATG	CGGGG	GAGAG	TAGTTT	TACAT	AGGGGT	TCATAGT	GAGGG	1331
Db	929	GKKKGK	GGKGGK	KKTKTK	TKKKKKK	KAD	AAAGK	TKKRA	AAADAA	ADWD	TAATKKK	988
Qy	1332	CTGTG	CCCTTG	TACAAA	1350							
Db	989	KKKKK	KKKTK	TKKKD	AAAA	1007						

RESULT 2	
CNS00LOO/c	
LOCUS	1101 bp DNA linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL068607
VERSION	AL068607.1 GI:4958689
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)
REFERENCE	Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <a href="http://www.fruitfly.org/TheBDGP/Drosophila">http://www.fruitfly.org/TheBDGP/Drosophila</a> melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at <a href="http://bacpac.med.buffalo.edu/drosophila_bac.htm">http://bacpac.med.buffalo.edu/drosophila_bac.htm</a> . Location/Qualifiers 1..1101 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR32D23"
FEATURES	source

seeds (large insert library)]. cDNA was prepared from polyA+ mRNA using SuperScript plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

## ORIGIN

Query Match 2.6%; Score 46.6; DB 6; Length 661;  
Best Local Similarity 55.2%; Pred. No. 0.097;  
Matches 91; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTTCAGATGCCATTTTCTCTCCAGCGTAACGGTGGCGGG 1641  
DB 323 GCGGCTACGCGCGCGCGGAGCGGTGGCGGTACGCGCGCGTGTAGAGGTGGCT 382

QY 1642 GTGGACGAGCGCGCGCGGAGGATCTGGCAAGATGGCTCGCGGGCGGTGCT 1701  
DB 383 ACGGCGGTGGCGCGCGCTACGCGCGGTGGCTACGCTGGCGGTGGGTGGCT 442

QY 1702 TCTTCTCGGTAAAGCTCTCTGGATACGTCTATCTGAAACGA 1746  
DB 443 ACTGCGCGGTGGCGCGCGCTACGCGCACTCCGAGGGGAACCTGA 487

## RESULT 4

CNS0073W 922 bp DNA linear GSS 03-JUN-1999  
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #  
DEFINITION BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

## ACCESSION

AL066784.1 GI:4945247

## VERSION

GSS.

## KEYWORDS

Drosophila melanogaster (fruit fly)

## SOURCE

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

## REFERENCE

1 (bases 1 to 922)

## AUTHORS

Genoscope.

## TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

## JOURNAL

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeogawa and Aaron Mammner in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

1..922  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR14D09"  
/clone\_lib="RPCI-98"  
/note="end : TET3"

## ORIGIN

Query Match 2.6%; Score 46.6; DB 9; Length 922;

Best Local Similarity 25.5%; Pred. No. 0.11;  
Matches 103; Conservative 112; Mismatches 188; Indels 1; Gaps 1;

QY 942 TTGCGACACCTTTCCCGCCCATGCCCTGAAATTCATATGAATAAATTAAGTCTTT 1001  
DB 456 YTCGCCCCCVCYCCCYCTTGGTGCTTTTCTTGTGTTTTTTTTTTTCTTTT 515

QY 1002 TTTATCACTTCGTAAAGTGTATTTATTTATTAAGGGTTAAGTGGGGTCTTTAAAT 1061  
DB 516 TTTTTTTTCTTTTCTGCTGKGTGTTTCTGCTGKGTGTTTCTGCTGKGTGTTTCTG 575

QY 1062 TAAATTCCTGATTTGTATACATACATGTTACACGATATTTGATTCCTGGTGTATATAC 1121  
DB 576 GGGKKTCTYKBTGTGTGTGKGGKGTGTTTGTGKKTGTGTTTGTGKKTGTGTTTGT 635

QY 1122 TGTTTT-TGCAACGAGTCCGAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTC 1180  
DB 636 TKTGKGGKGTGKGTGTTGGGKKTGTTGKGGKKTGKGGKKTGKGGKKTGKGTGTT 695

QY 1181 AGCCACAGCTGGTCTTTCTTTGTTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACA 1240  
DB 696 KGGKGGKKTGKGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 755

QY 1241 GGTGTTGGGGTAAAGTACCGGAGTGGTAGGAGAAGGGCTGGTTATGTTATGCGCGGAG 1300  
DB 756 KXGGKGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 815

QY 1301 GAGTAGTTTACATAGGGGTACATAGGTAGGGCTGTGGCCTTTGT 1344  
DB 816 KKKKKKTKTKKKKTKGGTKGGTKGGTKGGTKGGTKGGTKGGTKGGTKGGTKGGTK 859

RESULT 5  
LOCUS CA294389 497 bp mRNA linear EST 26-SEP-2003

DEFINITION SCGLV1012B06.g LV1 Saccharum officinarum cDNA clone SCGLV1012B06 5', mRNA sequence.

ACCESSION CA294389  
VERSION CA294389.1 GI:36056761

KEYWORDS EST.  
SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 497)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

CONTACT: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: [paradua@unicamp.br](mailto:paradua@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bccccenter.fcav.unesp.br>  
Plate: 012 row: B column: 06  
Seq primer: T7 Promoter Primer.

Location/Qualifiers  
1..497  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCGLV1012B06"  
/lab\_host="DH10B"  
/clone\_lib="LV1"  
/note="Organ: Etiolated leaves from in vitro grown seedlings; Vector: pSPort1; Site\_1: SalI; Site\_2: NotI; An unidirectional cDNA library generated from [Etiolated

leaves from in vitro grown seedlings). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 497;  
Best Local Similarity 54.5%; Pred. No. 0.17; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGTAAACGGTGGCGGG 1641  
Db 263 CGGCTACGGCGCGCGCGGTGAGCGGTGCGGCTACGCGCGCGGTGATGAGGTGGCT 322  
QY 1642 GTGACAGCAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 1701  
Db 323 ACGGCGGTGGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 382  
QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746  
Db 383 ACNCGCGCGGTGGCGCGCGGTACGCAACTCGAGGGGAACTGGA 427

RESULT 6

CA294459/c  
LOCUS SCGLV1012B06.b LV1 Saccharum officinarum cDNA clone SCGLV1012B06  
DEFINITION 3', mRNA sequence.  
ACCESSION CA294459  
VERSION CA294459.1 GI:36056985  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 598)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>  
Plate: 012 row: B column: 06  
Seq primer: SP6 Promoter primer.  
Location/Qualifiers  
1. .598  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCGLV1012B06"  
/lab\_host="DHI08"  
/clone\_lib="LV1"  
/note="Organ: Etiolated leaves from in vitro grown seedlings; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Etiolated leaves from in vitro grown seedlings]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the

FEATURES  
source

1. .598  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCGLV1012B06"  
/lab\_host="DHI08"  
/clone\_lib="LV1"  
/note="Organ: Etiolated leaves from in vitro grown seedlings; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Etiolated leaves from in vitro grown seedlings]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 598;  
Best Local Similarity 54.5%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGTAAACGGTGGCGGG 1641  
Db 489 GCGGTAAACNCGCGCGCGGTGAGCGGTGCGGCTACGCGCGCGGTGATGAGGTGGCT 430  
QY 1642 GTGACAGCAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 1701  
Db 429 ACGGCGGTGGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 370  
QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746  
Db 369 ACGGCGCGGTGGCGCGCGGTACGCAACTCGAGGGGAACTGGA 325

RESULT 7

CA108913/c  
LOCUS SCSGHR1067F11.b HR1 Saccharum officinarum cDNA clone SCSGHR1067F11  
DEFINITION 3', mRNA sequence.  
ACCESSION CA108913  
VERSION CA108913.1 GI:34962220  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 667)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>  
Plate: 067 row: F column: 11  
Seq primer: SP6 Promoter primer.  
Location/Qualifiers  
1. .667  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSGHR1067F11"  
/lab\_host="DHI0B"  
/clone\_lib="HR1"  
/note="Organ: seedlings inoculated with Herbaspirillum rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirillum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

FEATURES  
source

1. .667  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSGHR1067F11"  
/lab\_host="DHI0B"  
/clone\_lib="HR1"  
/note="Organ: seedlings inoculated with Herbaspirillum rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirillum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 598;  
Best Local Similarity 54.5%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGTAAACGGTGGCGGG 1641  
Db 489 GCGGTAAACNCGCGCGCGGTGAGCGGTGCGGCTACGCGCGCGGTGATGAGGTGGCT 430  
QY 1642 GTGACAGCAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 1701  
Db 429 ACGGCGGTGGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 370  
QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746  
Db 369 ACGGCGCGGTGGCGCGCGGTACGCAACTCGAGGGGAACTGGA 325

RESULT 7

CA108913/c  
LOCUS SCSGHR1067F11.b HR1 Saccharum officinarum cDNA clone SCSGHR1067F11  
DEFINITION 3', mRNA sequence.  
ACCESSION CA108913  
VERSION CA108913.1 GI:34962220  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 667)  
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>  
Plate: 067 row: F column: 11  
Seq primer: SP6 Promoter primer.  
Location/Qualifiers  
1. .667  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSGHR1067F11"  
/lab\_host="DHI0B"  
/clone\_lib="HR1"  
/note="Organ: seedlings inoculated with Herbaspirillum rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirillum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

FEATURES  
source

1. .667  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSGHR1067F11"  
/lab\_host="DHI0B"  
/clone\_lib="HR1"  
/note="Organ: seedlings inoculated with Herbaspirillum rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [seedlings inoculated with Herbaspirillum rubrisubalbicans]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

ORIGIN

Query Match 2.6%; Score 45.6; DB 6; Length 598;  
Best Local Similarity 54.5%; Pred. No. 0.19; Indels 0; Gaps 0;  
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGTAAACGGTGGCGGG 1641  
Db 489 GCGGTAAACNCGCGCGCGGTGAGCGGTGCGGCTACGCGCGCGGTGATGAGGTGGCT 430  
QY 1642 GTGACAGCAGCGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 1701  
Db 429 ACGGCGGTGGCGCGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGTGAGCGGT 370  
QY 1702 TCTTCTTCGTAACGCTCTTGGATACGTATCTGAAACGA 1746  
Db 369 ACGGCGCGGTGGCGCGCGGTACGCAACTCGAGGGGAACTGGA 325

Query Match 2.6%; Score 45.6; DB 6; Length 667;  
 Best Local Similarity 54.5%; Pred. No. 0.19;  
 Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

QY 1582 GCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCCAGCGGTAAAGTGGCGGG 1641  
 |||||  
 Db 459 GCGGNTACGGCGCGCGCGGTGAGCGGTGCGCGGTACGGCGCGGTGATGGAGGTGGCT 400  
 |||||  
 QY 1642 GTGGACGACGAGCGCGCGCGGAGGATCTGGCAAGATGGCTGCGGGCGCGGTGTCT 1701  
 |||||  
 Db 399 ACGGCGGTGCGCGCGCGGTACGGCGGTGGCTACGGTGGCGGTGGCGGTGGCT 340  
 |||||  
 QY 1702 TCTTCTTCGGTACACGCTCTTGGATACGTATATCTGAAACGA 1746  
 |||||  
 Db 339 ACGGCGCGGTGGCGCGGTACGGCACTCCGAGGGAACGTGA 295  
 |||||

RESULT 8  
 A1514058  
 LOCUS  
 DEFINITION GH27112.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH27112 5prime, mRNA sequence.

ACCESSION A1514058  
 VERSION A1514058.1 GI:4418120  
 KEYWORDS EST.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 561)  
 AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.

TITLE BDGP/HMI Drosophila EST Project  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Stapleton, M.  
 BDGP

Lawrence Berkeley National Lab  
 One Cyclotron Rd. Berkeley, CA 94720, USA  
 Fax: 510 486 6798  
 Email: <http://www.fruitfly.org/EST>, [est@fruitfly.berkeley.edu](mailto:est@fruitfly.berkeley.edu)  
 Plate: 271 row: A column: 12  
 High quality sequence stop: 488.

FEATURES  
 source  
 1..561  
 /organism="Drosophila melanogaster"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7227"  
 /clone="GH27112"  
 /sex="male and female"  
 /dev\_stage="adult"  
 /lab\_host="DHS - alpha"

/clone\_lib="GH Drosophila melanogaster head pOT2"  
 /notes="Organ: head; Vector: pOT2; Site: 1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."

ORIGIN  
 Query Match 2.6%; Score 45.4; DB 1; Length 561;  
 Best Local Similarity 58.5%; Pred. No. 0.21;  
 Matches 79; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1569 TATATCGAAGTGGCGGAGAGCGGGTGTGAAGATGCCATTTTCTTCTCCAGCGGT 1628  
 |||||  
 Db 426 TATTCGAGAGGTGGCGGAATCGCGGTGGAGGTGGCAATTCCTGGTGAGATAGCGGA 485  
 |||||

QY 1629 AACGGTGGCGGGTGGACGAGCAGCGCGCGGAGGATCTGCCAAGATGGCTGC 1688  
 |||||  
 Db 486 ATCGTGGCGCGCTGATTTGGTGGCGGAATCGGCGCGGAGGTGCCATTCCTGGTGA 545  
 |||||

QY 1689 GGGGCGGTGTCTTC 1703  
 |||||  
 Db 546 GCGCGTGAATCTGC 560  
 |||||

RESULT 9  
 CE373054/c

LOCUS  
 DEFINITION tigr-988-dog-17000362184725 Dog Library Canis familiaris genomic, genomic survey sequence.

ACCESSION CE373054  
 VERSION CE373054.1 GI:36596968  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 324)  
 AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 MEDLINE 22875432  
 PUBMED 14512627

COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: [ekirknes@tigr.org](mailto:ekirknes@tigr.org)  
 Class: shotgun.

FEATURES  
 source  
 1..324  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN  
 Query Match 2.6%; Score 45.2; DB 9; Length 324;  
 Best Local Similarity 54.9%; Pred. No. 0.2;  
 Matches 89; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 963 TCGCCCTGAATTTCCATATGAATAAATTACTCAGTCTTTTTTATCACCTTCGTAATCGTTT 1022  
 |||||  
 Db 317 TGACTTTTAACTCCCTTATAGATTCAGATAGAGCTTTCTTATCAACATGTATAGTAT 258  
 |||||

QY 1023 TTATTATTCAATTAAGGGTTAACTGGGGGTCTTTAAATAAATTTCTCTGAATTGTACAT 1082  
 |||||  
 Db 257 ATATCATATGTATAGATCTATATGTATTAAAGATTAAAGATCTACATCTTAAATATCTATAT 198  
 |||||

QY 1083 ACATGGTTACAGGATTTGTATTCTCTGTCGTATATACCTGT 1124  
 |||||  
 Db 197 CTATAGATATACCTATATATATCTCTGATGATATATCATAT 156  
 |||||

RESULT 10  
 AG034053

LOCUS  
 DEFINITION Pan troglodytes DNA, clone: PTB-009E13.F, genomic survey sequence.

ACCESSION AG034053  
 VERSION AG034053.1 GI:16560926  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes

REFERENCE 1  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 BAC end sequences of Library PTB

CE373054 324 bp DNA linear GSS 27-SEP-2003  
 tigr-988-dog-17000362184725 Dog Library Canis familiaris genomic, genomic survey sequence.

CE373054 GI:36596968  
 GSS.  
 Canis familiaris (dog)  
 Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 324)  
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 22875432  
 14512627

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: [ekirknes@tigr.org](mailto:ekirknes@tigr.org)  
 Class: shotgun.

FEATURES  
 source  
 1..324  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN  
 Query Match 2.6%; Score 45.2; DB 9; Length 324;  
 Best Local Similarity 54.9%; Pred. No. 0.2;  
 Matches 89; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 963 TCGCCCTGAATTTCCATATGAATAAATTACTCAGTCTTTTTTATCACCTTCGTAATCGTTT 1022  
 |||||  
 Db 317 TGACTTTTAACTCCCTTATAGATTCAGATAGAGCTTTCTTATCAACATGTATAGTAT 258  
 |||||

QY 1023 TTATTATTCAATTAAGGGTTAACTGGGGGTCTTTAAATAAATTTCTCTGAATTGTACAT 1082  
 |||||  
 Db 257 ATATCATATGTATAGATCTATATGTATTAAAGATTAAAGATCTACATCTTAAATATCTATAT 198  
 |||||

QY 1083 ACATGGTTACAGGATTTGTATTCTCTGTCGTATATACCTGT 1124  
 |||||  
 Db 197 CTATAGATATACCTATATATATCTCTGATGATATATCATAT 156  
 |||||

RESULT 10  
 AG034053

LOCUS  
 DEFINITION Pan troglodytes DNA, clone: PTB-009E13.F, genomic survey sequence.

ACCESSION AG034053  
 VERSION AG034053.1 GI:16560926  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes

REFERENCE 1  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 TITLE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 BAC end sequences of Library PTB

```

Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
Location/Qualifiers
1. 571
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wialc.pk003.e22"
/tissue_type="anthers"
/lab_host="DH108"
/clone_lib="wialc"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; Wheat (Triticum aestivum, Hi Line) immature anthers"

```

ORIGIN	Query Match	2.5%	Score 45;	DB 6;	Length 571;
	Best Local Similarity	57.4%;	Prod. NO. 0.27;		
	Matches 78;	Conservative	0; Mismatches	58; Indels	0; Gaps
QY	1576	GAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTTCACAGCGTAACGGTG	1635		
DB	250	GGAGCGGTGGCAGTGGAGGAGCGGTGGAGGCGGTCTGGAGAGCGGCAGCAGCGGAG	309		
QY	1636	GCGGGGTGGACGAGCCAGCGGGCGGGCGGAGGATCTGGCCAAATGGCTTCCGGGGCGC	1695		
DB	310	GCGGATCTGGAGGAGCGGCAGCGCGGAGCGGATCENNAGGAGGTGGCAGCAGCGCGC	369		
QY	1696	GTGCTTCTTCTTCGG	1711		
DB	370	GCGGGTCCGGCGGTGG	385		

RESULT 12	CA103262	linear	603 bp	mRNA	EST 23-SEP-2003				
LOCUS	SCEZHR1048D02	Saccharum officinarum cDNA clone SCEZHR1048D02							
DEFINITION	5', mRNA sequence.								
ACCESSION	CA103262	GI:34956569							
VERSION	CA103262.1	EST.							
KEYWORDS	Saccharum officinarum								
SOURCE	Saccharum officinarum								
ORGANISM	Saccharum officinarum								
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACMAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.								
REFERENCE	1 (bases 1 to 603)								
AUTHORS	Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda, P.								
TITLE	The libraries that made SUCEST								
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)								
COMMENT	Contact: Arruda P								

Email: parruda@unicamp.br  
 Clone distribution: clone distribution information can be found  
 through the Brazilian Clone Collection Center (BCCC) at  
<http://www.bccccenter.fcav.unesp.br>  
 Plate: 048 row: D column: 02  
 Seq primer: T7 Promoter Primer.  
 Location/Qualifiers  
     1. .603  
         /organism="Saccharum officinarum"  
         /mol\_type="mRNA"  
         /db\_xref="taxon:4547"  
         /clone="SCEZHR1048D02"  
         /lab\_host="DH10B"  
         /clone\_lib="HRI"  
         /notes="Organ: seedlings inoculated with Herbaespirillum"



in a sepharose CL-2B 40cm-column and fragments sizing into the between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://succest.lad.ic.unimac.br/public>"

## ORIGIN

Query Match 2.5%; Score 45; DB 6; Length 622;  
Best Local Similarity 54.5%;  
Pred. No. 0.28;  
Matches 90; Conservative 0; Mismatches 75; Indels

RESULT 14	CA198894	LOCUS	DEFINITION
-----------	----------	-------	------------

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

1 (bases 1 to 640)  
 Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.  
 The libraries that made SUCEST  
 Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 Contact: Arruda P  
 Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parruda@unicamp.br  
 Clone distribution: clone distribution information can  
 through the Brazilian Clone Collection Center (BCCC) a  
 http://www.bcccenter.fcav.unesp.br  
 Plate: 079 row: E column: 04  
 Sequencer primer: T7 Promoter Primer.

## FEATURES

1, 540  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCSGP1079E04"  
/lab\_host="DH10B"  
/clone\_libs="Fli18"  
/note="Organ: Inflorescence at beginning of development (1cm-long); Vector: pSPori1. Site of insertion: 5' noncoding region of the unidirectional cDNA library generated from poly(A)<sup>+</sup> mRNA from a 10-day-old inflorescence. The cDNA was prepared from poly(A)<sup>+</sup> mRNA using the RNeasy Plant System Kit (Invitrogen). The cDNA fragments were fractionated in a sepharose column and size fractionated between 0.8 and 1.2 kb. The cDNA fragments were directionally cloned into the vector construct. The source of RNA and library construction details are available at <http://www.ncbi.nlm.nih.gov/blast/blast.cgi?seqid=U000000000>.

```

/clone.lib="FLI"
/note="Organ: Inflorescence at beginning of development
(1cm-long); Vector: pSport1; Site_1: SalI; Site_2: NotI;
(1cm-long). An unidirectional cDNA library generated from
[Inflorescence at beginning of development (1cm-long)].
cDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucres.lad.ic.unimore.br/public"

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:39:01 ; Search time 7541 Seconds  
(without alignments)  
11080.878 Million cell updates/sec

**Title:** US-10-718-264-15  
**Perfect score:** 1767  
**Sequence:** 1 accagcgacttcgcacgcg.....agaagtgcctgtaagtatt 1767

Scoring table: IDENTITY\_NUC  
Gapox 10.0 . Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl : \*

```

1:  gb_ba:*
2:  gb_htg:*
3:  gb_in:*
4:  gb_cm:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1767	100.0	1767	6	AR4822255	AR4822255 Sequence
C	1767	100.0	1767	6	AR4822256	AR4822256 Sequence
3	1767	100.0	1767	6	AX0032374	AX0032374 Sequence
C	1767	100.0	1767	6	AX0032375	AX0032375 Sequence
5	1757.4	99.5	1767	14	AX0032184	AX0032184 Porcine C
6	1755.8	99.4	1767	14	AF201897	AF201897 Porcine C
7	1755.8	99.4	1767	14	AX321985	AX321985 Porcine C
8	1755.8	99.4	1767	14	AX321986	AX321986 Porcine C
9	1752.6	99.2	1767	14	AV256460	AV256460 Porcine C
10	1752.6	99.2	1767	14	AX321989	AX321989 Porcine C
11	1752.6	99.2	1767	14	AX322000	AX322000 Porcine C
12	1751	99.1	1767	14	AX188355	AX188355 Porcine C
13	1751	99.1	1767	14	AX321743	AX321743 Porcine C
14	1751	99.1	1767	14	AX321988	AX321988 Porcine C
15	1751	99.1	1767	14	AX321990	AX321990 Porcine C
16	1751	99.1	1767	14	AX321992	AX321992 Porcine C
17	1751	99.1	1767	14	AX321994	AX321994 Porcine C
18	1751	99.1	1767	14	AX321997	AX321997 Porcine C
19	1751	99.1	1767	14	AX322001	AX322001 Porcine C

20	1751	99.1	1767	14	AY322002	Porcine C
21	1751	99.1	1767	14	AY424405	Porcine C
22	1751	99.1	1767	14	AY536755	Porcine C
23	1751	99.1	1767	14	AY604430	Porcine C
24	1751	99.1	1767	14	AY613854	Porcine C
25	1749.4	99.0	1767	14	AY321987	Porcine C
26	1749.4	99.0	1767	14	AY321995	Porcine C
27	1749.4	99.0	1767	14	AY321998	Porcine C
28	1749.4	99.0	1767	14	AY321999	Porcine C
29	1747.8	98.9	1767	14	AY181945	Porcine C
30	1747.8	98.9	1767	14	AY321991	Porcine C
31	1747.8	98.9	1767	14	AY321996	Porcine C
32	1747.8	98.9	1767	14	AY424404	Porcine C
33	1746.2	98.8	1767	14	AY177626	Porcine C
34	1746.2	98.8	1767	14	AY256457	Porcine C
35	1746.2	98.8	1767	14	AY231316	Porcine C
36	1746.2	98.8	1767	14	AY536756	Porcine C
37	1746.2	98.8	1767	14	AY641542	Porcine C
38	1746.2	98.8	1767	14	AY651850	Porcine C
39	1741.4	98.6	1767	14	AY391729	Porcine C
40	1739.8	98.5	1767	14	AY596823	Porcine C
41	1736.6	98.3	1767	14	AY321982	Porcine C
42	1736.6	98.3	1767	14	AY321983	Porcine C
43	1735.6	98.2	1766	14	PC1293869	Porcine C
44	1735	98.2	1767	14	AY322003	Porcine C
45	1733	98.1	1778	14	AY3221993	Porcine C

## ALIGNMENTS

[illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.

QY 241 TTGTGAAGAAGCAGACCTTTTAAATAAGTGAAGTGTATTGGGTGCCCGCTGCCACATCG 300  
DB 241 TTGTGAAGAAGCAGACCTTTTAAATAAGTGAAGTGTATTGGGTGCCCGCTGCCACATCG 300  
QY 301 AGAAAGCGAAAGGAACAGATCAGCAGAGATAAAGAATACTGCAAGTAAAGAGCAACTTAC 360  
DB 301 AGAAAGCGAAAGGAACAGATCAGCAGAGATAAAGAATACTGCAAGTAAAGAGCAACTTAC 360  
QY 361 TGATGAGTGTGGAGCTCTAGATCTCAGGGACACGAGTGAACCTGTCTACTGCTGTGA 420  
DB 361 TGATGAGTGTGGAGCTCTAGATCTCAGGGACACGAGTGAACCTGTCTACTGCTGTGA 420  
QY 421 GTACCTTGTGGAGACGGGAGTCTGGTGAACCGTTGCAGAGCAGACACCTGTAAAGCTTG 480  
DB 421 GTACCTTGTGGAGACGGGAGTCTGGTGAACCGTTGCAGAGCAGACACCTGTAAAGCTTG 480  
QY 481 TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGGGAAGAAATGAGAGCGGTG 540  
DB 481 TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGGGAAGAAATGAGAGCGGTG 540  
QY 541 ATTGAAGACTAATGTACACGCTCATTTGTGGGCGCACCTGGGTGTTAAAGCAAAATGGG 600  
DB 541 ATTGAAGACTAATGTACACGCTCATTTGTGGGCGCACCTGGGTGTTAAAGCAAAATGGG 600  
QY 601 CTGCTAATTTTGCAGACCGGAAACCAATACTGGAACCACTAGAAACCAAGTGGTGG 660  
DB 601 CTGCTAATTTTGCAGACCGGAAACCAATACTGGAACCACTAGAAACCAAGTGGTGG 660  
QY 661 ATGTTACATGTTGAAGAAGTGTGTTATGATGACTTTTATGGCTGGCTGGCTGGG 720  
DB 661 ATGTTACATGTTGAAGAAGTGTGTTATGATGACTTTTATGGCTGGCTGGCTGGG 720  
QY 721 ATGATCTACTGAGACTGTGATCGATATCATCTGACTGATGAGACTAAAGTGGACTG 780  
DB 721 ATGATCTACTGAGACTGTGATCGATATCATCTGACTGATGAGACTAAAGTGGACTG 780  
QY 781 TACCTTTTGGCCGCGAGTATCTGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840  
DB 781 TACCTTTTGGCCGCGAGTATCTGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840  
QY 841 CCTCACTGTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTGTTGTTATTT 900  
DB 841 CCTCACTGTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTGTTGTTATTT 900  
QY 901 GGAAGATGCTACAGAAACAACTCCAGGAGGAGGGGCGAGTGTGTCACCTTTCCCGCC 960  
DB 901 GGAAGATGCTACAGAAACAACTCCAGGAGGAGGGGCGAGTGTGTCACCTTTCCCGCC 960  
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTTTATCACTTCGTAATGGT 1020  
DB 961 CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTTTATCACTTCGTAATGGT 1020  
QY 1021 TTTTATTATTCAATTAAGGGTTAAGTGGGGGTCTTTAAATTAATTTCTGAAATGTAC 1080  
DB 1021 TTTTATTATTCAATTAAGGGTTAAGTGGGGGTCTTTAAATTAATTTCTGAAATGTAC 1080  
QY 1081 ATACATGTTTACAGGATATTGTTATCTGCTGCTATATCTGTTTTCGAAAGCAGTGCC 1140  
DB 1081 ATACATGTTTACAGGATATTGTTATCTGCTGCTATATCTGTTTTCGAAAGCAGTGCC 1140  
QY 1141 GAGCGCTACGTTGTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
DB 1141 GAGCGCTACGTTGTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
QY 1201 GTTCTTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 1260  
DB 1201 GTTCTTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTACCG 1260  
QY 1261 GGAAGTGTAGGAGAGGCTGGTGTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320  
DB 1261 GGAAGTGTAGGAGAGGCTGGTGTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320  
QY 1321 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTTATCATCTTAAATAACAGCACTGGAGCC 1380

DB 1321 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTTATCATCTTAAATAACAGCACTGGAGCC 1380  
QY 1381 CACTCCCTGTGTCACCTTGGGTGATCGGGAGCAGGGCCAGAAATCAACCTTTCT 1440  
DB 1381 CACTCCCTGTGTCACCTTGGGTGATCGGGAGCAGGGCCAGAAATCAACCTTTCT 1440  
QY 1441 TATTCTGTAGTATTCAAAAGGCGACAGAGCGGGGTTGACCCCTCTCTGGGGAAGAAA 1500  
DB 1441 TATTCTGTAGTATTCAAAAGGCGACAGAGCGGGGTTGACCCCTCTCTGGGGAAGAAA 1500  
QY 1501 GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGCTTCTGACTGTGGTTG 1560  
DB 1501 GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGCTTCTGACTGTGGTTG 1560  
QY 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAAGTGCATTTTCTTCT 1620  
DB 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAAGTGCATTTTCTTCT 1620  
QY 1621 CCAGCGTAAACGTTGGCGGGGTGGACGAGCCAGGGCGCGGAGGATCTGGCCAAAG 1680  
DB 1621 CCAGCGTAAACGTTGGCGGGGTGGACGAGCCAGGGCGCGGAGGATCTGGCCAAAG 1680  
QY 1681 ATGCTCTCGGGCGGTGTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA 1740  
DB 1681 ATGCTCTCGGGCGGTGTCTTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA 1740  
QY 1741 AAACGAAAGAGTGCCTGTAAAGTATT 1767  
DB 1741 AAACGAAAGAGTGCCTGTAAAGTATT 1767

RESULT 2  
AR482256/c  
LOCUS AR482256 1767 bp DNA linear PAT 14-MAY-2004  
DEFINITION Sequence 19 from patent US 6703023.  
ACCESSION AR482256  
VERSION AR482256.1 GI:47244297  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1767)  
AUTHORS Jestin,A., Albina,E., Le Cann,P., Blanchard,P., Hutet,E.,  
Arnould,C., Truong,C., Mahe,D., Cariolet,R. and Madec,P.  
TITLE Circovirus sequences associated with piglet weight loss disease  
(PVD)  
JOURNAL Patent: US 6703023-A 19 09-MAR-2004;  
FEATURES Location/Qualifiers  
source 1..1767  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 1767; DB 6; Length 1767;  
Best Local Similarity 100.0%; Pred.No.0;  
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACAGCGCACTTCGGAGCGGAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 60  
DB 1767 ACCAGCGCACTTCGGAGCGGAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 1708  
QY 61 AGAAGATGAAGAAGCGGACCCCAACCCCATAAAAGTGGGTTCACCTCTGAATAATC 120  
DB 1707 AGAAGATGAAGAAGCGGACCCCAACCCCATAAAAGTGGGTTCACCTCTGAATAATC 1648  
QY 121 CTTCCGAAGCAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTTGATTATTTA 180  
DB 1647 CTTCCGAAGCAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTTGATTATTTA 1588  
QY 181 TTGTTGGCAGGAGGGTAAATGAGAGGAGCAACCTCACCTCCAGGGGTTGCTAATT 240  
DB 1587 TTGTTGGCAGGAGGGTAAATGAGAGGAGCAACCTCACCTCCAGGGGTTGCTAATT 1528

```
QY 241 TTGTGAAGAGCAGACTTTTAAATGAAGTGAAGTGGTATTGGGTGCCCGCTGCCACATCG 300
Db 1527 TTGTGAAGAGCAGACTTTTAAATGAAGTGAAGTGGTATTGGGTGCCCGCTGCCACATCG 1468
QY 301 AGAAAGCGAAAGGAAACAGATCAGCAGAGAAATAAGAAATACAGCAGTAAAGAGCGCACTTAC 360
Db 1467 AGAAAGCGAAAGGAAACAGATCAGCAGAGAAATAAGAAATACAGCAGTAAAGAGCGCACTTAC 1408
QY 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGCTACTGCTGTGA 420
Db 1407 TGATGGAGTGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGCTACTGCTGTGA 1348
QY 421 GTACCTTGTGTGAGAGCGGGAGTCTGGTGACCGTGTGAGAGCAGCACCTCTGTAAAGTTTG 480
Db 1347 GTACCTTGTGTGAGAGCGGGAGTCTGGTGACCGTGTGAGAGCAGCACCTCTGTAAAGTTTG 1288
QY 481 TCAGAAATTTCCGGGGTGGCTGAACTTTTGAAGAGTGAAGCGGGGAAATGCGAAGCGTG 540
Db 1287 TCAGAAATTTCCGGGGTGGCTGAACTTTTGAAGAGTGAAGCGGGGAAATGCGAAGCGTG 1228
QY 541 ATTGAAGACTAATGTACAGCTCATTTGTGGGCGCACCTGGGTGTGTAAGCAAAATGGG 600
Db 1227 ATTGAAGACTAATGTACAGCTCATTTGTGGGCGCACCTGGGTGTGTAAGCAAAATGGG 1168
QY 601 CTGCTAAATTTTCAGACCGGAAACACATACCTGAAACCACTAGAAACCAAGTGGTGGG 660
Db 1167 CTGCTAAATTTTCAGACCGGAAACACATACCTGAAACCACTAGAAACCAAGTGGTGGG 1108
QY 661 ATGTTTACCAGTGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 1107 ATGTTTACCAGTGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 1048
QY 721 ATGATCTACTGAGCTGTGTGATCATATCCATTGACTGTAGAGACTAAAGTGAACATG 780
Db 1047 ATGATCTACTGAGCTGTGTGATCATATCCATTGACTGTAGAGACTAAAGTGAACATG 988
QY 781 TACCTTTTTTGGCCGCGCAGTATTCGATTACCAGCAATCAGACCCCGTTGGAAATGGTACT 840
Db 987 TACCTTTTTTGGCCGCGCAGTATTCGATTACCAGCAATCAGACCCCGTTGGAAATGGTACT 928
QY 841 CCTCAACTGCTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT 900
Db 927 CCTCAACTGCTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT 868
QY 901 GGAAGATGCTACAGAAACATCCACGAGGAAGGGGCGCAGTTCGTACCCCTTTCCCCC 960
Db 867 GGAAGATGCTACAGAAACATCCACGAGGAAGGGGCGCAGTTCGTACCCCTTTCCCCC 808
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTTTATCACTTCGTAATGGT 1020
Db 807 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTTTATCACTTCGTAATGGT 748
QY 1021 TTTTATTATTCAATTAAGGGTTAAGTGGGGGCTTTTAAATTAATTTCTGAAATGTATC 1080
Db 747 TTTTATTATTCAATTAAGGGTTAAGTGGGGGCTTTTAAATTAATTTCTGAAATGTATC 688
QY 1081 ATACATGGTTACAGGATATTTGATTTCTGGTGTATATCTGTTTTTCGAAACGAGTGGC 1140
Db 687 ATACATGGTTACAGGATATTTGATTTCTGGTGTATATCTGTTTTTCGAAACGAGTGGC 628
QY 1141 GAGGCTTACGTGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCAGCTGGTTTCTTTT 1200
Db 627 GAGGCTTACGTGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCAGCTGGTTTCTTTT 568
QY 1201 GTTGTGTGGTGAAGTAAATCAATAGTGAATCTAGGACAGAGTTTGGGGGTAAAGTACCG 1260
Db 567 GTTGTGTGGTGAAGTAAATCAATAGTGAATCTAGGACAGAGTTTGGGGGTAAAGTACCG 508
QY 1261 GGAAGTGGTGAAGAGCGGTGGTTATGGTATGGCGGAGGAGTAGTTTACATAGGGGTC 1320
Db 507 GGAAGTGGTGAAGAGCGGTGGTTATGGTATGGCGGAGGAGTAGTTTACATAGGGGTC 448
```

```
QY 1321 ATAGGTGAGGCGCTGTGGCCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 447 ATAGGTGAGGCGCTGTGGCCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 388
QY 1381 CACTCCCTCTGCACCCCTGGGTGATCGGGAGCAGGCCAGAAATCAACCTTTAAACCTTTCT 1440
Db 387 CACTCCCTCTGCACCCCTGGGTGATCGGGAGCAGGCCAGAAATCAACCTTTAAACCTTTCT 328
QY 1441 TATTCTGTAGTATTCAAAGGGCAAGAGCGGGGTTTGAACCCCTCTCTGGGGGAAGAAA 1500
Db 327 TATTCTGTAGTATTCAAAGGGCAAGAGCGGGGTTTGAACCCCTCTCTGGGGGAAGAAA 268
QY 1501 GTCAATTAATATTGAATCTCATCATGTCCACGCCAGGAGGGCGTTCGACTGTGGTTCCG 1560
Db 267 GTCAATTAATATTGAATCTCATCATGTCCACGCCAGGAGGGCGTTCGACTGTGGTTCCG 208
QY 1561 CTTGACAGTATATCCGAAGGTCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTTCT 1620
Db 207 CTTGACAGTATATCCGAAGGTCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTTCT 148
QY 1621 CCAGCGGTAAACGGTGGCGGGGTGGAACAGCCAGGGCGGGCGGAGGATCTGGCCAAAG 1680
Db 147 CCAGCGGTAAACGGTGGCGGGGTGGAACAGCCAGGGCGGGCGGAGGATCTGGCCAAAG 88
QY 1681 ATGGCTGGGGGCGGTGTCTTCTTCTCGTAAGCCCTCTCTGATAGCTCATATCTGA 1740
Db 87 ATGGCTGGGGGCGGTGTCTTCTTCTCGTAAGCCCTCTCTGATAGCTCATATCTGA 28
QY 1741 AAACGAAAGAAAGTGCCTGTAAGTATT 1767
Db 27 AAACGAAAGAAAGTGCCTGTAAGTATT 1

RESULT 3
AX003274
LOCUS AX003274
DEFINITION Sequence 9 from Patent WO9929871.
ACCESSION AX003274
VERSION AX003274.1 GI:9927098
KEYWORDS Porcine circovirus
SOURCE Porcine circovirus
ORGANISM Porcine circovirus
REFERENCE 1 Hutet,E., Albin,E., Arnould,C., Cariolet,R., Jestin,A., Le,C.P.,
AUTHORS Mader,P., Mahe,D., Blanchard,P. and Truong,C.
TITLE Circovirus sequences related to piglet weight loss disease (pwd)
JOURNAL Patient: WO 9929871-A 9 17-JUN-1999;
HUTET EVELYNE (FR); ALBINA EMMANUEL (FR); ARNAULD CLAIRE (FR);
CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
FRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
CATHERINE (FR); VETERINAIRES ET ALIMENTAIRES C (FR)
FEATURES
source
1. .1767
/organism="Porcine circovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:46221"
/note="Circovirus MAP type B-Brin polarit + (5'-3')"
```

## ORIGIN

```
Query Match 100.0%; Score 1767; DB 6; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCAGGGCACTTCGGCAGCGGCGAGCACTTCGGCAGCAGCCTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGGGCACTTCGGCAGCGGCGAGCACTTCGGCAGCAGCCTCAGCAGCAACATGCCAGCA 60
QY 61 AGAAGAAATCGAAGAACGGACCCCAACCCCATAAAAGGTGGGTGTTCACTCTGAATAATC 120
Db 61 AGAAGAAATCGAAGAACGGACCCCAACCCCATAAAAGGTGGGTGTTCACTCTGAATAATC 120
QY 121 CTTCCGAAGACGAGCGCAAGAAATAACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
```

```
Db 121 |TTTCGAGACGAGCGCAAGAAATACGGATCTTCCATATCCCTATTGTAATTTTA 180
Qy 181 |TTGTTGGCCAGAGGGTAAATAGGAAGAGACGAAACCTCACTCAGGGGTTTCGTAATT 240
Db 181 |TTGTTGGCCAGAGGGTAAATAGGAAGAGACGAAACCTCACTCAGGGGTTTCGTAATT 240
Qy 241 |TTGTGAAGAACGAGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
Db 241 |TTGTGAAGAACGAGACTTTTAAATGAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
Qy 301 |AGAAAGCGAAAGAAACAGATCAGCAGAAATAAGAAATACCTGAGTAAAGAGGCAACTTAC 360
Db 301 |AGAAAGCGAAAGAAACAGATCAGCAGAAATAAGAAATACCTGAGTAAAGAGGCAACTTAC 360
Qy 361 |TGATGGAGTGTGGAGCTCTAGATCTCAGGGAACAAGAGTGAACCTGTCTACTGTGTA 420
Db 361 |TGATGGAGTGTGGAGCTCTAGATCTCAGGGAACAAGAGTGAACCTGTCTACTGTGTA 420
Qy 421 |GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTGACAGAGCAGACACCTGTAAAGTTTG 480
Db 421 |GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTGACAGAGCAGACACCTGTAAAGTTTG 480
Qy 481 |TCAGAAATTTCCGGGCTGGCTGAACCTTTTGAAGTGAAGGCGGAAATGACAGAGCGTG 540
Db 481 |TCAGAAATTTCCGGGCTGGCTGAACCTTTTGAAGTGAAGGCGGAAATGACAGAGCGTG 540
Qy 541 |ATTGGAAGACTAATGTACACGTATGTTGGGCGCACCTGGGTGTGGTAAAGCAATGGG 600
Db 541 |ATTGGAAGACTAATGTACACGTATGTTGGGCGCACCTGGGTGTGGTAAAGCAATGGG 600
Qy 601 |CTGCTAAATTTGACAGACCGGAAACACATATCTGAAACCACTAGAAACCAAGTGGTGG 660
Db 601 |CTGCTAAATTTGACAGACCGGAAACACATATCTGAAACCACTAGAAACCAAGTGGTGG 660
Qy 661 |ATGTTATCATGTTGAAGAGTGTGTTATGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 661 |ATGTTATCATGTTGAAGAGTGTGTTATGATGACTTTTATGGCTGGCTGCCCTGGG 720
Qy 721 |ATGATCTACTGAGCTGTGATCGATATCATCTGACTGTAGAGACTAAAGTGGAACTG 780
Db 721 |ATGATCTACTGAGCTGTGATCGATATCATCTGACTGTAGAGACTAAAGTGGAACTG 780
Qy 781 |TACCTTTTGGCCGCGAGTATCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 840
Db 781 |TACCTTTTGGCCGCGAGTATCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 840
Qy 841 |CCTCAACTGTCTCCAGCTGTAGAGCTCTTTATCGAGGATTAATCTTCTTGGTATTTT 900
Db 841 |CCTCAACTGTCTCCAGCTGTAGAGCTCTTTATCGAGGATTAATCTTCTTGGTATTTT 900
Qy 901 |GGAAGATGCTACAGAAACAACTCCAGGAGGAGGGCCAGTCTGTCACCCCTTCCCGCC 960
Db 901 |GGAAGATGCTACAGAAACAACTCCAGGAGGAGGGCCAGTCTGTCACCCCTTCCCGCC 960
Qy 961 |CATGCCCTGAATTTCCATATGAATAATTAATCTAGTCTTTTATCACTTCGTAATGGT 1020
Db 961 |CATGCCCTGAATTTCCATATGAATAATTAATCTAGTCTTTTATCACTTCGTAATGGT 1020
Qy 1021 |TTTTATTATTCATTAAGGTTAAGTGGGGGTCTTTAAATTAATCTCTGAAATGTAC 1080
Db 1021 |TTTTATTATTCATTAAGGTTAAGTGGGGGTCTTTAAATTAATCTCTGAAATGTAC 1080
Qy 1081 |ATACATGGTTACAGGATTAATGTTCTGCTGATATATCTGTTTCGACGAGTGGC 1140
Db 1081 |ATACATGGTTACAGGATTAATGTTCTGCTGATATATCTGTTTCGACGAGTGGC 1140
Qy 1141 |GAGCCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Db 1141 |GAGCCCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
Qy 1201 |GTTGTTGGTTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
```

```
Db 1201 GTTGTGTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
Qy 1261 GGAATGTTAGGAGAGGGCTGGGTTATGTTATGCGGGAGGAGTAGTTTACATAGGGTTC 1320
Db 1261 GGAATGTTAGGAGAGGGCTGGGTTATGTTATGCGGGAGGAGTAGTTTACATAGGGTTC 1320
Qy 1321 ATAGTGAAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACCTGGAGCC 1380
Db 1321 ATAGTGAAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATTAACAGCACCTGGAGCC 1380
Qy 1381 CACTCCCTCTGCACCTCGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTTCT 1440
Db 1381 CACTCCCTCTGCACCTCGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTTCT 1440
Qy 1441 TATTCTGTAGTATTCAAAGGACAGAGCGGGGTTTGAACCCCTCTCGGGGGAAGAAA 1500
Db 1441 TATTCTGTAGTATTCAAAGGACAGAGCGGGGTTTGAACCCCTCTCGGGGGAAGAAA 1500
Qy 1501 GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGGTTCTGACTGTGGTTTCG 1560
Db 1501 GTCAATTAATTTGAATCTCATGTCCACCGCCAGGAGGGGTTCTGACTGTGGTTTCG 1560
Qy 1561 CTTGACAGTATATCCGAAAGTGGCGGAGAGCGGGTGTGAAAGATGCAATTTTTCCTTCT 1620
Db 1561 CTTGACAGTATATCCGAAAGTGGCGGAGAGCGGGTGTGAAAGATGCAATTTTTCCTTCT 1620
Qy 1621 CCAGCGGTAAACGTTGGCGGGGTGGAGCAGCAGGCGCGCGGAGGATCTGGCCAAAG 1680
Db 1621 CCAGCGGTAAACGTTGGCGGGGTGGAGCAGCAGGCGCGCGGAGGATCTGGCCAAAG 1680
Qy 1681 ATGCTCTCGGGCGGGTGTCTTCTTCTCGGTAAACGCTCTTGGATACCTCATATCTGA 1740
Db 1681 ATGCTCTCGGGCGGGTGTCTTCTTCTCGGTAAACGCTCTTGGATACCTCATATCTGA 1740
Qy 1741 AAACGAAAGAAAGTCCGCTGTAAGTATT 1767
Db 1741 AAACGAAAGAAAGTCCGCTGTAAGTATT 1767

RESULT 4
AX003275/c
LOCUS Sequence 10 from Patent WO9929871.
DEFINITION AX003275
ACCESSION AX003275
VERSION AX003275.1 GI:9927099
KEYWORDS Porcine circovirus
SOURCE Porcine circovirus
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1
AUTHORS Hutet, E., Albina, E., Arnaud, C., Cariolet, R., Jestin, A., Le, C.P.,
Maded, F., Mahe, D., Blanchard, P. and Truong, C.
TITLE Circovirus sequences related to piglet weight loss disease (pwd)
JOURNAL Patent: WO 9929871-A 10 17-JUN-1999;
HUTET EVELYNE (FR); ALBINA EMANUEL (FR); ARNAUD CLAIRE (FR);
CARIOLET ROLAND (FR); JESTIN ANDRE (FR); LE CANN PIERRE (FR); MADEC
FRANCOIS (FR); MAHE DOMINIQUE (FR); BLANCHARD PHILIPPE (FR); TRUONG
CATHERINE (FR); VETERINAIRES ET ALIMENTAIRES C (FR)

FEATURES
source
1. .1767
/organism="Porcine circovirus"
/mol_type="unassigned DNA"
/db_xref="taxon:46221"
/note="Circovirus MAP type B-Brin polarit - (5'-3')"
```

```
Query Match 100.0%; Score 1767; DB 6; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACAGCGCACTTCGGCAGCGGAGCAGCTCGGAGCAGCACTCGGAGCAACATGCCAGCA 60
Db 1767 ACCAGCGCACTTCGGCAGCGGAGCAGCTCGGAGCAGCAACATGCCAGCA 1708
```

QY 61 AGAAGATGGAAGACGCGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGAATATC 120  
Db 1707 AGAAGATGGAAGACGCGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGAATATC 1648  
QY 121 CTTCCGAAGACGAGCGCAAGAAAATA CGGGATCTTTCCAAATATCCCTATTTGATTTTAA 180  
Db 1647 CTTCCGAAGACGAGCGCAAGAAAATA CGGGATCTTTCCAAATATCCCTATTTGATTTTAA 1588  
QY 181 TTGTTGGCGAGGAGGTATGAGGAGACGACCACTCACTCCAGGGGTTCGCTAATT 240  
Db 1587 TTGTTGGCGAGGAGGTATGAGGAGACGACCACTCACTCCAGGGGTTCGCTAATT 1528  
QY 241 TTGTTGAAGACGAGCTTTTAAATAAGTGAAGTGGTATTTGGGTCCCGCTGCCACATCG 300  
Db 1527 TTGTTGAAGACGAGCTTTTAAATAAGTGAAGTGGTATTTGGGTCCCGCTGCCACATCG 1468  
QY 301 AGAAGCGAAGGAAACAGATCAGCAGAGATAAAGAAATATCGCAGTAAAGAGCAACTTAC 360  
Db 1467 AGAAGCGAAGGAAACAGATCAGCAGAGATAAAGAAATATCGCAGTAAAGAGCAACTTAC 1408  
QY 361 TGATCGAGTGTGAGCTCTAGATCTCAGGACACGAGTGACCTGTCTACTGCTGTA 420  
Db 1407 TGATCGAGTGTGAGCTCTAGATCTCAGGACACGAGTGACCTGTCTACTGCTGTA 1348  
QY 421 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTTGACAGCAGCACCTGTAAAGCTTTG 480  
Db 1347 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTTGACAGCAGCACCTGTAAAGCTTTG 1288  
QY 481 TCAGAAATTTCCCGGGCTGGCTGAATTTTGAAGTGAAGCGGAAATGCAAGAGCGTG 540  
Db 1287 TCAGAAATTTCCCGGGCTGGCTGAATTTTGAAGTGAAGCGGAAATGCAAGAGCGTG 1228  
QY 541 ATTGAAGACTAATGTACACGTCAATGTGGGCGACCTGGGTGTTGTTAAAGCAATGGG 600  
Db 1227 ATTGAAGACTAATGTACACGTCAATGTGGGCGACCTGGGTGTTGTTAAAGCAATGGG 1168  
QY 601 CTGCTAAATTTTCAGACCCGGAACACATCTCGAAACCACTAGAAACAGTGGTGGG 660  
Db 1167 CTGCTAAATTTTCAGACCCGGAACACATCTCGAAACCACTAGAAACAGTGGTGGG 1108  
QY 661 ATGGTTTACCATGGTGAAGAGTGGTGTGTTATGATGACTTTTATGGTGGCTGCCCTGGG 720  
Db 1107 ATGGTTTACCATGGTGAAGAGTGGTGTGTTATGATGACTTTTATGGTGGCTGCCCTGGG 1048  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAGGTGGAACCTG 780  
Db 1047 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTAAGGTGGAACCTG 988  
QY 781 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGTTACT 840  
Db 987 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTTGGAAATGTTACT 928  
QY 841 CTTCAACTCTGTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900  
Db 927 CTTCAACTCTGTCTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 868  
QY 901 GGAAGAAATGCTACAGAAACAAATCCAGGAGAGGGGGCCAGTTCGTACCCCTTCCCCCC 960  
Db 867 GGAAGAAATGCTACAGAAACAAATCCAGGAGAGGGGGCCAGTTCGTACCCCTTCCCCCC 808  
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTATGCT 1020  
Db 807 CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTATGCT 748  
QY 1021 TTTTATTTTTCATTAAAGGTTAAGTGGGGGTCTTTTAAATTAATTTCTCTGAATTTGATC 1080  
Db 747 TTTTATTTTTCATTAAAGGTTAAGTGGGGGTCTTTTAAATTAATTTCTCTGAATTTGATC 688  
QY 1081 ATACATGGTTACACGATATGTTATTCCTGGTGGTATATCTGTTTTTCGAACGCAATGCC 1140  
Db 687 ATACATGGTTACACGATATGTTATTCCTGGTGGTATATCTGTTTTTCGAACGCAATGCC 628

QY 1141 GAGCCCTACGTGCTGTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
Db 627 GAGCCCTACGTGCTGTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 568  
QY 1201 GTTCTTTGTTGGAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGGTAAAGTACCG 1260  
Db 567 GTTCTTTGTTGGAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGGTAAAGTACCG 508  
QY 1261 GGAAGTGTAGGAGAGGGCTGGGTTATGGTATGCGGAGGAGTAGTTTATCATAGGGGTC 1320  
Db 507 GGAAGTGTAGGAGAGGGCTGGGTTATGGTATGCGGAGGAGTAGTTTATCATAGGGGTC 448  
QY 1321 ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC 1380  
Db 447 ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC 388  
QY 1381 CACTCCCTGTCAACAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 1500  
Db 387 CACTCCCTGTCAACAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 268  
QY 1441 TATTCTGTAGTATTCAAAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 1500  
Db 327 TATTCTGTAGTATTCAAAGGGCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAAA 268  
QY 1501 GTCAATTAATATTGAATCTCATCTGTCACCGCCAGGAGGGCTTCTGACTGTGGTTCCG 1560  
Db 267 GTCAATTAATATTGAATCTCATCTGTCACCGCCAGGAGGGCTTCTGACTGTGGTTCCG 208  
QY 1561 CTTGACAGTATATCCGAGGTCGCGAGAGCGGGTGTGAAGATGCCATTTTCTCTTCT 1620  
Db 207 CTTGACAGTATATCCGAGGTCGCGAGAGCGGGTGTGAAGATGCCATTTTCTCTTCT 148  
QY 1621 CCAGCGGTAAACGGTGGCGGGGTGACAGCAGCGCGGGCGGGCGGAGGATCGGCCAAG 1680  
Db 147 CCAGCGGTAAACGGTGGCGGGGTGACAGCAGCGCGGGCGGGCGGAGGATCGGCCAAG 88  
QY 1681 ATGGCTCGGGGGGGTGTCTTTCTTTCGTAAGCCCTCTCTGTAAGTACGTATCTGA 1740  
Db 87 ATGGCTCGGGGGGGTGTCTTTCTTTCGTAAGCCCTCTCTGTAAGTACGTATCTGA 28  
QY 1741 AAACGAAAGAGTGGCTGTAAATTT 1767  
Db 27 AAACGAAAGAGTGGCTGTAAATTT 1  
RESULT 5  
AY321984  
LOCUS Porcine circovirus 2 strain Pd3, complete genome.  
DEFINITION Porcine circovirus 2  
ACCESSION AY321984  
VERSION AY321984.1 GI:32478760  
KEYWORDS Porcine circovirus 2  
SOURCE Porcine circovirus 2  
ORGANISM Porcine circovirus 2  
REFERENCE 1 (bases 1 to 1767)  
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,  
Eveno, E., Mader, F. and Jestin, A.  
TITLE Molecular characterization of Porcine circovirus type 2 isolates  
from post-weaning multisystemic wasting syndrome-affected and  
non-affected pigs  
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)  
JOURNAL 14769887  
PUBMED 2 (bases 1 to 1767)  
REFERENCE de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,  
Eveno, E., Mader, F. and Jestin, A.  
AUTHORS Direct Submission  
TITLE Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French  
JOURNAL Food Safety Agency, Bp 53, Ploufragan 22 440, France  
FEATURES Location/Qualifiers  
source  
1. .1767  
/organism="Porcine circovirus 2"  
/virion



```
/mol_type="genomic DNA"
/strain="Pd3"
/db_xref="taxon:85708"
/notes="type: 2"
51..995
/codon_start=1
/product="replicase"
/protein_id="AAP83595.1"
/db_xref="GI:32478761"
/translation="MPSKNGRSGPQPHKRWFTLNNPSEDERKKIRDLPISLDFVFI
VGEENEGRTPLHQLGFANFQKTNKVMYLGARCHIEKAGTKQONKBYCSKGN
LLMCKGPRSGDLSSTAVSLLESGSLVTAQHPVTFRNFRGLAELLKVSQKM
QKRDKNVNIQVGPCCGSKWAANFADPETTVKPKRNKMDGVGHVEVVIDDFY
GWLPHDLLRLCDRYPLIVETKGTVPFLARSILITSNQTPLEWYSSTA VPAVEALVR
RITSLVFNKATBOSTEGGQFVTLSPPCPEFFEYNY"
complement (1033..1734)
/codon_start=1
/product="capsid"
/protein_id="AAP83596.1"
/db_xref="GI:32478762"
/translation="MTYPRRRYRRHRPRSHLQILRRBPLVHPHRYRWRKNGI
FNTLSRTFGTVTKRTVTTPSWADMMRFNINDFLPFGGSPRSPVPPFYRIRKVK
VEFWPCSPITQDGRGVSSAVIDLDNFVTKATALTDYDYNYSRSHVITPPFSHSRY
PTPKVLDSTIDYFPNNKRNQLRLQTAGNVHDVGLTAFENSIYDQBYNIRVTMY
VQPRENLKDPPLNP"
```

## ORIGIN

```
Query Match 99.5%; Score 1757.4; DB 14; Length 1767;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1761; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCAGCGCATTCCGACGGCGAGCACCTCGCGACGACCTCAGCAGCAACATGCCAGCA 60
DB 1 ACCAGCGCATTCCGACGGCGAGCACCTCGCGACGACCTCAGCAGCAACATGCCAGCA 60

QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGTGTCTACTCTGAATATC 120
DB 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGTGTCTACTCTGAATATC 120

QY 121 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCATATCCCTATTTGATTTTGA 180
DB 121 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCATATCCCTATTTGATTTTGA 180

QY 181 TTGTTGGCGAGGAGGTATGAGGAGGACGAAACACCTCACCTCAGCGGGTTCGTAAT 240
DB 181 TTGTTGGCGAGGAGGTATGAGGAGGACGAAACACCTCACCTCAGCGGGTTCGTAAT 240

QY 241 TTGTAAGAGCAGACCTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300
DB 241 TTGTAAGAGCAGACCTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG 300

QY 301 AGAAGCGAAGAACAGATCAGCAGATAAAGATACCTGAGTAAAGAGGCAACTTAC 360
DB 301 AGAAGCGAAGAACAGATCAGCAGATAAAGATACCTGAGTAAAGAGGCAACTTAC 360

QY 361 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGTGTA 420
DB 361 TGAATGAGTGTGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTGTGTA 420

QY 421 GTACCTTTGTAAGAGCGGAGTCTGGTGACCGTTTCAGAGCAGACCCCTGTAAGCTTG 480
DB 421 GTACCTTTGTAAGAGCGGAGTCTGGTGACCGTTTCAGAGCAGACCCCTGTAAGCTTG 480

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGAAATGCGAAGCGGTG 540
DB 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAGCGGAAATGCGAAGCGGTG 540

QY 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTCGGTGTGGTAAAGCAATGG 600
DB 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTCGGTGTGGTAAAGCAATGG 600

QY 601 CTGCTAATTTTGCAGACCGGAAACCATCTCTGGAACCATCTAGAACCAAGTGGTGG 660
DB 601 CTGCTAATTTTGCAGACCGGAAACCATCTCTGGAACCATCTAGAACCAAGTGGTGG 660
```

```
Db 601 CTGCTAATTTTGCAGACCGGAAACCATCTCTGGAACCATCTAGAACCAAGTGGTGG 660
QY 661 ATGGTTTACCATTGGTGAAGAAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGG 720
DB 661 ATGGTTTACCATTGGTGAAGAAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGG 720
QY 721 ATGATCTACTGAGACTGTGTGATTCATTCATCTGATAGAGACTAAAGTGGAACTG 780
DB 721 ATGATCTACTGAGACTGTGTGATTCATTCATCTGATAGAGACTAAAGTGGAACTG 780
QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTGGGAATGGTACT 840
DB 781 TACCTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTGGGAATGGTACT 840
QY 841 CTTCAACTCTCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 841 CTTCAACTCTCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
QY 901 GGAAGATGCTACAGAACAATCCACGGAGGAGGGGGCCAGTTCGTCACCCCTTCCCC 960
DB 901 GGAAGATGCTACAGAACAATCCACGGAGGAGGGGGCCAGTTCGTCACCCCTTCCCC 960
QY 961 CATGCCCTGAAATTTCCATATGAAATAAATTAATCTGAGTCTTTTATCACTTCGTATGGT 1020
DB 961 CATGCCCTGAAATTTCCATATGAAATAAATTAATCTGAGTCTTTTATCACTTCGTATGGT 1020
QY 1021 TTTTATTAATTAAGGTAAAGTGGGGTCTTTAAATAAATTAATCTCTGAATGTGAC 1080
DB 1021 TTTTATTAATTAAGGTAAAGTGGGGTCTTTAAATAAATTAATCTCTGAATGTGAC 1080
QY 1081 ATACATGGTTACAGGATATTTCTTCTGCTGATATCTGTTTTCGAAACGACGTGC 1140
DB 1081 ATACATGGTTACAGGATATTTCTTCTGCTGATATCTGTTTTCGAAACGACGTGC 1140
QY 1141 GAGGCTCTGCTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
DB 1141 GAGGCTCTGCTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200
QY 1201 GTTGTGTTGGTGAAGTAATCAATAGTAAATCTAGACAGGTTTGGGGTAAAGTACCG 1260
DB 1201 GTTGTGTTGGTGAAGTAATCAATAGTAAATCTAGACAGGTTTGGGGTAAAGTACCG 1260
QY 1261 GAGTGTAGAGGAGGCTGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1261 GAGTGTAGAGGAGGCTGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1320
QY 1321 ATAGTGTAGGCTGTGGCTTTTGTACAAAGTTATCATCTAATAAATCAACAGCCTGGAGCC 1380
DB 1321 ATAGTGTAGGCTGTGGCTTTTGTACAAAGTTATCATCTAATAAATCAACAGCCTGGAGCC 1380
QY 1381 CACTCCCTGTCACTGGGTGATCGGGAGGAGGGCCAGAAATCAACCTTAACTTTCT 1440
DB 1381 CACTCCCTGTCACTGGGTGATCGGGAGGAGGGCCAGAAATCAACCTTAACTTTCT 1440
QY 1441 TATTTCTGATTTTCAAGGSCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAGAA 1500
DB 1441 TATTTCTGATTTTCAAGGSCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAGAA 1500
QY 1501 GTCAATTAATATTGAATCTCATCTGTCACCGCCAGAGGGGCTTCTGACTGTGGTTCG 1560
DB 1501 GTCAATTAATATTGAATCTCATCTGTCACCGCCAGAGGGGCTTCTGACTGTGGTTCG 1560
QY 1561 CTTGACAGTATATCCGAAGGTGCGGAGGAGCGGCTTGAAGATGCCATTTTCTTCT 1620
DB 1561 CTTGACAGTATATCCGAAGGTGCGGAGGAGCGGCTTGAAGATGCCATTTTCTTCT 1620
QY 1621 CCAGCGGTAAACGTTGGGGGGTGGACGAGCCAGGGCGGGCGGAGGAGTCTCGCCAA 1680
DB 1621 CCAGCGGTAAACGTTGGGGGGTGGACGAGCCAGGGCGGGCGGAGGAGTCTCGCCAA 1680
QY 1681 ATGGCTCGGGGGGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
DB 1681 ATGGCTCGGGGGGGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
```



```
QY 1741 AAACGAAGAAGTGGCTGTAAGTATT 1767
|||||
Db 1741 AAACGAAGAAGTGGCTGTAAGTATT 1767

RESULT 6
AF201897 1767 bp DNA circular VRL 20-DEC-2000
LOCUS Porcine circovirus type 2, complete genome.
DEFINITION Porcine circovirus type 2, complete genome.
ACCESSION AF201897
VERSION AF201897.1 GI:11907587
KEYWORDS
SOURCE
ORGANISM Porcine circovirus 2
VIRUSES; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE 1 (bases 1 to 1767)
AUTHORS Wellenberg,G.J., Pesch,S., Berendsen,F.W., Steverink,P.J.G.M.,
Hunneman,W., Van der Vorst,T.J.K., Peperkamp,N.H.M.T.,
Ohlinger,V.F., Schippers,R., Van Oirschot,J.T. and de Jong,M.F.
TITLE Isolation and characterization of porcine circovirus type 2 from
pigs showing signs of post-weaning multisystemic wasting syndrome
in The Netherlands
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1767)
AUTHORS Pesch,S. and Ohlinger,V.F.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Virology and Molecular Epidemiology,
BioScreen European Veterinary Disease Management Center GmbH, 11
Mendelstr., Muenster, NRW 48149, Germany
FEATURES
Location/Qualifiers
1..1767
/organism="Porcine circovirus 2"
/mol_type="genomic DNA"
/strain="24657 NL"
/db_xref="taxon:85708"
/country="Netherlands"
/complement(join(1731..1767,1..92))
/gene="ORF9"
/complement(join(1731..1767,1..92))
/gene="ORF9"
/note="4.6 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF9"
/protein_id="AAG41234.1"
/db_xref="GI:11907596"
/translation="WGLGSASSILLAGHVAEVLPRCCRSALVILTAHFFRFQI"
51..995
/gene="ORF1"
51..995
/gene="ORF1"
/note="putative Rep protein; 35.8 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF1"
/protein_id="AAG41226.1"
/db_xref="GI:11907588"
/translation="MPSKNGSGGPPHQRVFTLNNPSEDERKKIRDLPLSLDFYFI
VGEENEGRTPLHQFANFVKQTFNKYKVLGARCHIEKAGTDQKNKYCSKEGN
LLMECAPRSQGRSLLSTAVSTLLSGSLVTAEQHPVTVFRNFRGLAELLKVSQKM
OKRDWNTVHVIVGPPCGCKSKWAANFADPETTYKPRNKWDGYPHGEVVVIDDFY
GWLWDDLRLCQDPLTVETKGTVPFLARSILITSNQTPLEWTSSTAVPAVEALYR
RTSLVFNKNAQTEQSGGQFVTLSPPCPEPPEYINY"
complement(357..671)
/gene="ORF3"
complement(357..671)
/gene="ORF3"
/note="11.9 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF3"
/protein_id="AAG41228.1"

/db_xref="GI:11907590"
/translation="MTTIPPLVSRWFVCGFRVCKIKSPPFAFTTTPRPHNDVYISLPI
TLHFPAHFQKFSQPAEISDKRYRVLCCNGHQTALOOGTHSSHQVTPLSLRSRSLTL
HQ"
complement(386..565)
/gene="ORF4"
complement(386..565)
/gene="ORF4"
/note="6.5 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF4"
/protein_id="AAG41229.1"
/db_xref="GI:11907591"
/translation="MTCTLVQSRFCIFPLTFKSSASPRKFLTNVTGCCSATVTRLPL
SNKVLTAVDRLSLRCP"
complement(688..753)
/gene="ORF8"
complement(688..753)
/gene="ORF8"
/note="2.3 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF8"
/protein_id="AAG41233.1"
/db_xref="GI:11907595"
/translation="MDIDHTVSDHPRAASHKSHQ"
complement(989..1033)
/gene="ORF11"
complement(989..1033)
/gene="ORF11"
/note="1.8 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF11"
/protein_id="AAG41230.1"
/db_xref="GI:11907592"
/translation="MNNKNHYEVIKKTO"
complement(1033..1734)
/gene="ORF2"
complement(1033..1734)
/gene="ORF2"
/note="27.8 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF2"
/protein_id="AAG41227.1"
/db_xref="GI:11907589"
/translation="MTYPRRYRRRRHPRSHLQQLRRRPWLVPRIHRYWRKNGI
FNRLSRFTGYTKRTVTTPSWAVDMRMFINDFLPPGGSGNPRSPVPEYIRKVK
VEFWPCSPITQDGRGVGSSAVILDNFTVKATALTALTYPVVYSSRHTITQPPSYHSRY
ETPKPVLDSIDYFQPNKRNQLWLRLQTAGNVHDVGLGTAFENSIYDQEVNIRVTMY
VQPREFLKDPPLNP"
complement(1521..1610)
/gene="ORF6"
complement(1521..1610)
/gene="ORF6"
/note="3.1 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF6"
/protein_id="AAG41231.1"
/db_xref="GI:11907593"
/translation="NASSTPASPPSDILSSEPPQERPPGRWT"
1523..1630
/gene="ORF10"
1523..1630
/gene="ORF10"
/note="4.1 kDa"
/codon_start=1
/evidence=not_experimental
/product="ORF10"
/protein_id="AAG41235.1"
```

```
/db_xref="GI:11907597"
/translation="MSTAQEGVLTVRLTVVVKVRRRLVKNPFFLLQR"
1681..1740
/gene="ORF7"
1681..1740
/gene="ORF7"
/note="1.9 kDa"
/codon_start=1
/evidence=not experimental
/product="ORF7"
/protein_id="AAG41232.1"
/db_xref="GI:11907594"
/translation="MAAGAVSSPVPPIRHI"

ORIGIN
Query Match          99.4%; Score 1755.8; DB 14; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1760; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ACCAGCGACATTGGCGAGCGGCGAGCACCTCGCGAGCACCTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGCGACATTGGCGAGCGGCGAGCACCTCGCGAGCACCTCAGCAGCAACATGCCAGCA 60

Qy 61 AGAAGATGGAAGACGGACCCCAACCCCAATAAAAGGTGGGTCTACTCTGAATAATC 120
Db 61 AGAAGATGGAAGACGGACCCCAACCCCAATAAAAGGTGGGTCTACTCTGAATAATC 120

Qy 121 CTTCCGAGACGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180
Db 121 CTTCCGAGACGCGGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180

Qy 181 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAAACACCTCACCTCAGGGGTTTCGCTAAT 240
Db 181 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAAACACCTCACCTCAGGGGTTTCGCTAAT 240

Qy 241 TTGTGAAGACGACATTTTAAATGAAAGTGAAGTGTATTTGGGTGCCCGCTGCCACATCG 300
Db 241 TTGTGAAGACGACATTTTAAATGAAAGTGAAGTGTATTTGGGTGCCCGCTGCCACATCG 300

Qy 301 AGAAGCGAAGAAACAGATCAGCAGAAATGAAGATATCGCAGTAAAGAGGCACTTAC 360
Db 301 AGAAGCGAAGAAACAGATCAGCAGAAATGAAGATATCGCAGTAAAGAGGCACTTAC 360

Qy 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTACTGTCTGA 420
Db 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTACTGTCTGA 420

Qy 421 GTACCTTGTGGAGACGGGAGTCTGGTGAACCGTTGACAGACGACACCTGTAACTG 480
Db 421 GTACCTTGTGGAGACGGGAGTCTGGTGAACCGTTGACAGACGACACCTGTAACTG 480

Qy 481 TCAGAAATTTCCGGGGCTGGCTGAACCTTTTGAAGTGAAGGGAATGCAAGCGTG 540
Db 481 TCAGAAATTTCCGGGGCTGGCTGAACCTTTTGAAGTGAAGGGAATGCAAGCGTG 540

Qy 541 ATTGAAGACATACTGACAGCTATTGTGGGCGACCTGGGTGTGTTAAAGCAATGCG 600
Db 541 ATTGAAGACATACTGACAGCTATTGTGGGCGACCTGGGTGTGTTAAAGCAATGCG 600

Qy 601 CTGCTAAATTTTCAGACCCGGAACCAATCTAGGAAACCACTTGAAGAAACAAAGTGGTGG 660
Db 601 CTGCTAAATTTTCAGACCCGGAACCAATCTAGGAAACCACTTGAAGAAACAAAGTGGTGG 660

Qy 661 ATGTTACATGTTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGGCTGGG 720
Db 661 ATGTTACATGTTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGGCTGGG 720

Qy 721 ATGATCTACTGAGACTGTGATCGATATCAATTCAGTGTAGAGACTAAAGTGAACCTG 780
Db 721 ATGATCTACTGAGACTGTGATCGATATCAATTCAGTGTAGAGACTAAAGTGAACCTG 780

Qy 781 TACCTTTTGGCCCGCAGTATTTGATTAACGCAATCAGACCCCGTGGAAATGGTACT 840
Db 781 TACCTTTTGGCCCGCAGTATTTGATTAACGCAATCAGACCCCGTGGAAATGGTACT 840
```

```
Db 781 TACCTTTTGGCCCGCAGTATTTGATTAACGCAATCAGACCCCGTGGAAATGGTACT 840
Qy 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTTACTCTCTGTTGTTT 900
Db 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTTACTCTCTGTTGTTT 900
Qy 901 GGAAGAAATGCTACAGAAACAATCCACGGAGGAGGCGGCGTCTGCTCACTTTCCTCC 960
Db 901 GGAAGAAATGCTACAGAAACAATCCACGGAGGAGGCGGCGTCTGCTCACTTTCCTCC 960
Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAAGTCTTTTATCACTTCGTAATGGT 1020
Db 961 CATGCCCTGAATTTCCATATGAATAAATTAAGTCTTTTATCACTTCGTAATGGT 1020
Qy 1021 TTTTATTTATTTAAGGTTAAGTGGGGTCTTTAAATTAATTAATTTCTCTGAATTTGAC 1080
Db 1021 TTTTATTTATTTAAGGTTAAGTGGGGTCTTTAAGATTAATTAATTTCTCTGAATTTGAC 1080
Qy 1081 ATACATGTTTACACGGATATTGTTATCTCTGCTGATATATCTGTTTTCGAAACGAGTGC 1140
Db 1081 ATACATGTTTACACGGATATTGTTATCTCTGCTGATATATCTGTTTTCGAAACGAGTGC 1140
Qy 1141 GAGSCCTACGTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTT 1200
Db 1141 GAGSCCTACGTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTT 1200
Qy 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
Db 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG 1260
Qy 1261 GGAGTGTAGGAGAGGCTGGGTATTGTTATGGCGGAGGAGTGTATTACATAGGGGTC 1320
Db 1261 GGAGTGTAGGAGAGGCTGGGTATTGTTATGGCGGAGGAGTGTATTACATAGGGGTC 1320
Qy 1321 ATAGTGAGGCTGTGCGCTTTGTTACAAAGTATATCATCTAAATATACAGCCTGGAGCC 1380
Db 1321 ATAGTGAGGCTGTGCGCTTTGTTACAAAGTATATCATCTAGAAATACAGCCTGGAGCC 1380
Qy 1381 CACTCCCTCTGTCACCTGGGTGATCGGGAGCAGGCGGAGGAGGAGGAGGAGGAGGAGG 1440
Db 1381 CACTCCCTCTGTCACCTGGGTGATCGGGAGCAGGCGGAGGAGGAGGAGGAGGAGG 1440
Qy 1441 TATTCTGTAGTATTCAAAGGCGACAGACGCGGGGTTTGACCCCTCTCTGGGGAGAGAA 1500
Db 1441 TATTCTGTAGTATTCAAAGGCGACAGACGCGGGGTTTGAGCCCTCTCTGGGGAGAGAA 1500
Qy 1501 GTCAATTAATTTGAATCTCATGTCCACGCGCCAGAGGCGGTTCTGACTGTGGTTCG 1560
Db 1501 GTCAATTAATTTGAATCTCATGTCCACGCGCCAGAGGCGGTTCTGACTGTGGTTCG 1560
Qy 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCAATTTTCTTTCT 1620
Db 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCAATTTTCTTTCT 1620
Qy 1621 CCAGCGGTAAAGTGGCGGGGTGACAGCAGGCGGCGGCGGCGGAGGATCTGGCCAAAG 1680
Db 1621 CCAGCGGTAAAGTGGCGGGGTGACAGCAGGCGGCGGCGGCGGAGGATCTGGCCAAAG 1680
Qy 1681 ATGCTCTGGGGCGGCTGTTCTTCTTCTGTAACGCTCTCTGGATACGTCATATCTGA 1740
Db 1681 ATGCTCTGGGGCGGCTGTTCTTCTTCTCCGGTAAACGCTCTCTGGATACGTCATATCTGA 1740
Qy 1741 AAACGAAAGAGTGGCTGTAAGTATT 1767
Db 1741 AAACGAAAGAGTGGCTGTAAGTATT 1767
```

```
RESULT 7
AV321985
LOCUS      1767 bp      DNA      circular VRL 11-FEB-2004
DEFINITION Porcine circovirus 2 strain Fd13, complete genome.
ACCESSION  AV321985
VERSION     AV321985.1 GI:32478763
```

KEYWORDS	Porcine circovirus 2
SOURCE	Porcine circovirus 2
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE	1 (bases 1 to 1767)
AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.
TITLE	Molecular characterization of Porcine circovirus type 2 isolates from post-weaning multisystemic wasting syndrome-affected and non-affected pigs
JOURNAL	J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
PUBMED	14769887
REFERENCE	2 (bases 1 to 1767)
AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.
TITLE	Direct Submission
JOURNAL	Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French Food Safety Agency, BP 53, Ploufragan 22 440, France
FEATURES	Location/Qualifiers
source	1. .1767
	/organism="Porcine circovirus 2"
	/vireon
	/mol_type="genomic DNA"
	/strain="Fd13"
	/db_xref="taxon:85708"
	/note="type: 2"
	51. .995
CDS	/codon_start=1
	/product="replicase"
	/protein_id="AAP83597.1"
	/db_xref="GI:32478764"
	/translations="MPSKNKGRSGQPQHKRVFTLNPSEDERKKIRDLPISLFDYFI
	LVMECAQSGQSRDLSLSTAVSLTLESGSLVVAEOHPVTFRNFRGLAEILLKVSQKM
	QKRDKNVHVIYVPGCGSKSNANPADPTTMYKPKRWKWDGVBHGEVVIDDFY
	GWLPDILLCDRIYPLVETIKGTGVPFLARSLIITSNPTELYWSSYTAUVAEALYR
	RITSLVFNKATQPTFEEGGQFVTLSPPCPEFFYEINY"
	complement (1033. .1734)
	/codon_start=1
	/product="capsid"
	/protein_id="AAP83598.1"
	/db_xref="GI:32478765"
	/translations="MTYPRRYRRRRHRRPESHIGQILRRPWLHVRHRYWRKRNKI
	FNTRLSTFGYTVKTRTTPVPSWADMMRENIINDFLPPGGSNPRSPVPEYIRKVK
	VEFPPCSPITQGDGVGSSAVILDDNPTKATLTALYDPVYVNSRRTITQPFYSHRY
	FTPKPVLDSITDYFQPNKNQWLRLQTAGNVHDVGLGTAFENSIVDQEYINRVMTY
	VQRFENLKDPLNP"
CDS	
ORIGIN	
Query Match	99.4%; Score 1755.8; DB 14; Length 1767;
Best Local Similarity	99.6%; Pred. No. 0;
Matches 1760; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
Qy	1 ACCAGCGCATTTCGGCAGCGCAGCAGCCTCGGACGACCTCGGACGACCAATGCCAGCA 60
Db	1 ACCAGCGCATTTCGGCAGCGCAGCAGCCTCGGACGACCTCGGACGACCAATGCCAGCA 60
Qy	61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTTCACCTCTGAATAATC 120
Db	61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAGTGGGTTCACCTCTGAATAATC 120
Qy	121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAAATCCCTATTTGATTATTTTA 180
Db	121 CTTCCGAAGACGAGCGCAAGAAATA CGGGATCTTCCAAATCCCTATTTGATTATTTTA 180
Qy	181 TTGTTGGCAGGAGGTTAATGAGGAAGGACCAACCTCACCTCCAGGGGTTCCGCTAATT 240
Db	181 TTGTTGGCAGGAGGTTAATGAGGAAGGACCAACCTCACCTCCAGGGGTTCCGCTAATT 240
Qy	241 TTGTGAAGACGAGACTTTTATAAAGTGAAGTGGTATTTGGGTGCCGCTGCCACATCG 300
Db	241 TTGTGAAGACGAGACTTTTATAAAGTGAAGTGGTATTTGGGTGCCGCTGCCACATCG 300

Db 1381 CACTCCCTGTCAACCTGGTGATCGGGAGCAGGCCAGAAATCAACCTTAACCTTTCT 1440  
Qy 1441 TATTCGTAGTATCAAAAGGCACAGAGCGGGGTTTACCCCTCTCTGGGGAGAGAA 1500  
Db 1441 TATTCGTAGTATCAAAAGGCACAGAGCGGGGTTTACCCCTCTCTGGGGAGAGAA 1500  
Qy 1501 GTCAATTAATATGAATCTCATCATGTCCACCGCCAGAGGGCGTTCTGACTGTGGTTCTG 1560  
Db 1501 GTCAATTAATATGAATCTCATCATGTCCACCGCCAGAGGGCGTTCTGACTGTGGTTCTG 1560  
Qy 1561 CTTGACAGTATATCGAAGGTGCGGAGAGCGGGTGTGGAAGATGCGCAATTTTCTTTCT 1620  
Db 1561 CTTGACAGTATATCGAAGGTGCGGAGAGCGGGTGTGGAAGATGCGCAATTTTCTTTCT 1620  
Qy 1621 CCAGCGGTAAAGTGGCGGGGTGACAGCAGCGGGCGGGCGGGAGGATCTGGCCAG 1680  
Db 1621 CCAGCGGTAAAGTGGCGGGGTGACAGCAGCGGGCGGGCGGGAGGATCTGGCCAG 1680  
Qy 1681 ATGGCTGGGGGGCGGTCTTCTTCTTTCGTTAAGCGCTCTCTTGATACGTCATATCTGA 1740  
Db 1681 ATGGCTGGGGGGCGGTCTTCTTCTTTCGTTAAGCGCTCTCTTGATACGTCATATCTGA 1740  
Qy 1741 AAACGAAAGAGTGGCTGTGAAGTATT 1767  
Db 1741 AAACGAAAGAGTGGCTGTGAAGTATT 1767

RESULT 8  
AY321986  
LOCUS Porcine circovirus 2 strain Fd4, complete genome. 1767 bp DNA circular VRL 11-FEB-2004  
DEFINITION Porcine circovirus 2 strain Fd4, complete genome.  
ACCESSION AY321986  
VERSION AY321986.1 GI:32478766  
KEYWORDS Porcine circovirus 2  
SOURCE Porcine circovirus 2  
ORGANISM Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE 1 (bases 1 to 1767)  
AUTHORS de Boisseson,C., Beven,V., Bigarre,L., Thierry,R., Rose,N.,  
Eveno,E., Madec,P. and Jestin,A.  
TITLE Molecular characterization of Porcine circovirus type 2 isolates  
from post-weaning multisystemic wasting syndrome-affected and  
non-affected pigs  
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)  
14769887  
REFERENCE 2 (bases 1 to 1767)  
AUTHORS de Boisseson,C., Beven,V., Bigarre,L., Thierry,R., Rose,N.,  
Eveno,E., Madec,P. and Jestin,A.  
TITLE Direct Submission  
JOURNAL Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French  
Food Safety Agency, BP 53, Ploufragan 22 440, France  
FEATURES  
source  
1..1767  
/organism="Porcine circovirus 2"  
/product="replicase"  
/locus="F4"  
/mol\_type="genomic DNA"  
/strain="Fd4"  
/db\_xref="taxon:85708"  
/note="type: 2"  
51..995  
/codon\_start=1  
/product="replicase"  
/protein\_id="AAP83599.1"  
/db\_xref="GI:32478767"  
/translation="MPTKNGRSGPQHKRWVFTLNPNSEDERKKIRDLPLISLFDYFI  
VGEENEGRTPLHQLGFANFVKQTFNKRWYLGARHIEKAGTDQONKEYCSKEGN  
LLMECGAPRSQSDLSLSTVAEQLHSPVTFVRFNRLAEILKVSQGM  
QKRDKNVHVIQPGCGSKSMAANFADPETTYKPKRWKWDYHGEVWVDDFY  
GRLPDDLLRLCDYPLTVETKGTVPPLASLITSNQTFLEWYSSTAVPAVALIR  
RITSLVFWKNATEGSTREGGFVTLSPPCPFPEYIN"  
complement (1033..1734)  
/codon\_start=1

/product="capsid"  
/protein\_id="AAP83600.1"  
/db\_xref="GI:32478768"  
/translation="MTYPRRYRRRRHPRSHLQGLLRRLVHPRHVRWRKNGI  
FNRLSKRTGTGTVKRTVTPSWADVMRFNINDFLPPGGSPRSVPFYRIRKVK  
VFWPSPITQDGRGVSSAVIDNDNFRTATATYDPYVYNSRHTITQFPFSYHSRY  
FTPKPVLDSITDYFQPNKRNQLWLRLQTAGNVHVLGLTAFENSIDYQSYNRTVMY  
VQPREFLNKDPLNP"  
ORIGIN  
Query Match 99.4%; Score 1755.8; DB 14; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1760; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 ACCAGCCGACCTTCGGAGCGGAGCACCCTCGGAGCAGCCTCAGCAGCAACATGCCACCA 60  
Db 1 ACCAGCCGACCTTCGGAGCGGAGCACCCTCGGAGCAGCCTCAGCAGCAACATGCCACCA 60  
Qy 61 AGAAGATGGAAGAAGCGGACCCCAACCCCAATAAAGTGGGTGTTCACTCTGAATAATC 120  
Db 61 AGAAGATGGAAGAAGCGGACCCCAACCCCAATAAAGTGGGTGTTCACTCTGAATAATC 120  
Qy 121 CTTCCGAAGCAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180  
Db 121 CTTCCGAAGCAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTAA 180  
Qy 181 TTGTTGGCAGGAGGGTAATGAGGAAGGAGCAACACCTCACCTCCAGGGTTCGCTAAT 240  
Db 181 TTGTTGGCAGGAGGGTAATGAGGAAGGAGCAACACCTCACCTCCAGGGTTCGCTAAT 240  
Qy 241 TTGTGAAGAAGCAGACCTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG 300  
Db 241 TTGTGAAGAAGCAGACCTTTTAAATAAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG 300  
Qy 301 AGAAGCGAAAGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCACTTAC 360  
Db 301 AGAAGCGAAAGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCACTTAC 360  
Qy 361 TGATGAGTGTGGAGCTCTAGATCTCAGGAGCAACGGAGTACCTCTCTACTCTCTGA 420  
Db 361 TGATGAGTGTGGAGCTCTAGATCTCAGGAGCAACGGAGTACCTCTCTACTCTCTGA 420  
Qy 421 GTACCTTTGTTGGAGCGGGAGTCTGGTGACCGTTGAGAGCAGCACCCTGTAACTGTTG 480  
Db 421 GTACCTTTGTTGGAGCGGGAGTCTGGTGACCGTTGAGAGCAGCACCCTGTAACTGTTG 480  
Qy 481 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAGCGGGAATAATCAGAGCGTG 540  
Db 481 TCAGAAATTTCCGGGGCTGGCTGAATTTTGAAGTGAGCGGGAATAATCAGAGCGTG 540  
Qy 541 ATTGGAAGACTTAATGTACAGTCAATTTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600  
Db 541 ATTGGAAGACTTAATGTACAGTCAATTTGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600  
Qy 601 CTGCTAATTTTGCAGACCCCGGAAACCAATCTAGAAACCACTTAGAAACCAAGTGGTGG 660  
Db 601 CTGCTAATTTTGCAGACCCCGGAAACCAATCTAGAAACCACTTAGAAACCAAGTGGTGG 660  
Qy 661 ATGGTTACCATGTGGAAGAGTGGTGTGTTATGATGATCTTTTATGGCTGGCTGGCTGG 720  
Db 661 ATGGTTACCATGTGGAAGAGTGGTGTGTTATGATGATCTTTTATGGCTGGCTGGCTGG 720  
Qy 721 ATGATCTACTGAGACTGTGATCGATATCCATTTGCTAGTAGACTTAAAGTGGAACTG 780  
Db 721 ATGATCTACTGAGACTGTGATCGATATCCATTTGCTAGTAGACTTAAAGTGGAACTG 780  
Qy 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTGGAACTGACT 840  
Db 781 TACCTTTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTGGAACTGACT 840  
Qy 841 CTTCACTGCTGCTCCAGCTGTAGAGCTCTTTTATCGAGAGTACTCTCTCGTATTTT 900  
Db 841 CTTCACTGCTGCTCCAGCTGTAGAGCTCTTTTATCGAGAGTACTCTCTCGTATTTT 900



```
QY 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATATCTGCAGTAAAGAGGCAACTTAC 360
Db 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATATCTGCAGTAAAGAGGCAACTTAC 360
QY 361 TGATGGAGTGTGGAGCTCCTAGATCTCTCAGGACCAACGAGTACCTCTCTACTCTGTA 420
Db 361 TGATGGAGTGTGGAGCTCCTAGATCTCTCAGGACCAACGAGTACCTCTCTACTCTGTA 420
QY 421 GTACCTTGTGGAGAGCGGAGTCTGTGTGACCCGTTCAGAGCAGCACCCTGTACGTTTG 480
Db 421 GTACCTTGTGGAGAGCGGAGTCTGTGTGACCCGTTCAGAGCAGCACCCTGTACGTTTG 480
QY 481 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAAGCGGAAATGTCAGAAAGCGTG 540
Db 481 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAAGCGGAAATGTCAGAAAGCGTG 540
QY 541 ATTGGAAGACTAATGTATACACGCTCAATTTGTGGGCGCACCTGGTGTGTAAGCAAAATGGG 600
Db 541 ATTGGAAGACTAATGTATACACGCTCAATTTGTGGGCGCACCTGGTGTGTAAGCAAAATGGG 600
QY 601 CTGCTAATTTTGCAGACCCGGAACCACTACTGGAACCAACCTAGAAACCAAGTGGTGG 660
Db 601 CTGCTAATTTTGCAGACCCGGAACCACTACTGGAACCAACCTAGAAACCAAGTGGTGG 660
QY 661 ATGGTTACCATGTGTGAAGAGTGTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
Db 661 ATGGTTACCATGTGTGAAGAGTGTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCAATTCGACTGTAGAGACTAAAGGTGGAAGCTG 780
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCAATTCGACTGTAGAGACTAAAGGTGGAAGCTG 780
QY 781 TACCTTTTGGCCGCGAGTATCTGATACCAATCAGCAATCAGACCCGCTGGAATGGTACT 840
Db 781 TACCTTTTGGCCGCGAGTATCTGATACCAATCAGCAATCAGACCCGCTGGAATGGTACT 840
QY 841 CCTCACTGCTGCTCCAGCTGTGAGAGCTTTTATCGGAGGATTAATCTCTGTTGTTATTT 900
Db 841 CCTCACTGCTGCTCCAGCTGTGAGAGCTTTTATCGGAGGATTAATCTCTGTTGTTATTT 900
QY 901 GGAAGATGTCTACAGAAACAACTCCAGGAGGAGGCGGCACTTCGTACACCTTTCCCGCC 960
Db 901 GGAAGATGTCTACAGAAACAACTCCAGGAGGAGGCGGCACTTCGTACACCTTTCCCGCC 960
QY 961 CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
Db 961 CATGCCCTGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 TTTTATTATTCTAATAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAAT 1080
Db 1021 TTTTATTATTCTAATAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAAT 1080
QY 1081 ATACATGTTTACAGGATATTGTATTCCTGCTGATATCTGTTTTCGAAACGAGTGCC 1140
Db 1081 ATACATGTTTACAGGATATTGTATTCCTGCTGATATCTGTTTTCGAAACGAGTGCC 1140
QY 1141 GAGGCTACGTGCTCTACATTTCCAGCAGTTGTAGTCTCAGCCACAGCTGGTTCITTT 1200
Db 1141 GAGGCTACGTGCTCTACATTTCCAGCAGTTGTAGTCTCAGCCACAGCTGGTTCITTT 1200
QY 1201 GTTGTTCGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
Db 1201 GTTGTTCGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
QY 1261 GGAGTGTAGGAGAGGCTGGTTATGTTATGTCGGGAGGAGTAGTTTACATAGGGTCT 1320
Db 1261 GGAGTGTAGGAGAGGCTGGTTATGTTATGTCGGGAGGAGTAGTTTACATAGGGTCT 1320
QY 1321 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1321 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
```

```
QY 1381 CACTCCCCCTGTACCCCTGGGTGATCGGGAGCAGAGGCCAGAAATTCACCTTAACCTTTCT 1440
Db 1381 CACTCCCCCTGTACCCCTGGGTGATCGGGAGCAGAGGCCAGAAATTCACCTTAACCTTTCT 1440
QY 1441 TATTCTGTAGTATTCAAAGGACACAGCGGGGTTTGACCCCTCCCTGGGGGAGAAA 1500
Db 1441 TATTCTGTAGTATTCAAAGGACACAGCGGGGTTTGAGCCCTCCCTGGGGGAGAAA 1500
QY 1501 GTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 1501 GTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
QY 1561 CTTGACAGTATATCCGAAAGTGTGGAGAGCGGGTGTGAAGATGCAATTTTCTTTCT 1620
Db 1561 CTTGACAGTATATCCGAAAGTGTGGAGAGCGGGTGTGAAGATGCAATTTTCTTTCT 1620
QY 1621 CAGCGGTAAACGTTGGCGGGGTGGAGAGCAGAGCGCGCGCGGAGGATCTGGCCAAAG 1680
Db 1621 CAGCGGTAAACGTTGGCGGGGTGGAGAGCAGAGCGCGCGCGGAGGATCTGGCCAAAG 1680
QY 1681 ATGCTGCGGGGCGGTGTCTTCTTCTCGGTAAACGCTCTTGGATACCTCATATCTGA 1740
Db 1681 ATGCTGCGGGGCGGTGTCTTCTTCTCGGTAAACGCTCTTGGATACCTCATATCTGA 1740
QY 1741 AAACGAAAGAAAGTGTGCGCTGTAAGTATT 1767
Db 1741 AAACGAAAGAAAGTGTGCGCTGTAAGTATT 1767

RESULT 10
AY321989
LOCUS Porcine circovirus 2 strain Fd12, complete genome.
DEFINITION Porcine circovirus 2 strain Fd12, complete genome.
ACCESSION AY321989
VERSION AY321989.1 GI:32478775
SOURCE Porcine circovirus 2
ORGANISM Porcine circovirus 2
REFERENCE 1 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
JOURNAL J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
PUBMED 14769887
REFERENCE 2 (bases 1 to 1767)
AUTHORS de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
FEATURES
source
1. .1767
/organism="Porcine circovirus 2"
/virus
/mol_type="genomic DNA"
/strain="Fd12"
/db_xref="taxon:85708"
/notes="type: 2"
51. .995
/codon_start=1
/product="replicase"
/protein_id="AA983605.1"
/db_xref="GI:32478776"
/translation="MPSKNGRSGPQPHKRWFTLNNPSDERKKLRDLPLSLFDYFI
VGSENEGRTPLHQGFANFKQTKWYLGARCHIEKAKGTDOONKEYCSKEGN
LLMECGAPRSGQSDLSAVSTLLSGSLVTVAEQHPVTFRNFRGLAELLKVSQKM
QKDWKTNVHIVGPPCGCKSKWAANFADPTTWWKPRNKWDGVBGEVWVDDFY
GWLPMDDLRLCDRLPLTVETKGTVPFLARSILITSNQTPLEWYSTAVPAVEALYR
RTLSLVPWKNAATQSGTEGGQFVTLSPCPPEFYELN"
complement (1033. .1734)
CDS
CDS
```





```

1 (bases 1 to 1767)
de Boissesson, C., Beven, V., Bigarre, L., Thierly, R., Rose, N.,
Eveno, E., Mader, F. and Jestin, A.
TITLE
Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
JOURNAL
14769887
2 (bases 1 to 1767)
de Boissesson, C., Beven, V., Bigarre, L., Thierly, R., Rose, N.,
Eveno, E., Mader, F. and Jestin, A.
TITLE
Direct Submission
Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
JOURNAL
Location/Qualifiers
FEATURES
source
1. 1767
/organism="Porcine circovirus 2"
/virus
/mol_type="genomic DNA"
/strain="rdl"
/db_xref="taxon:85708"
/notes="type: 2"
51..995
/codon_start=1
/product="replicase"
/protein_id="AAP83627.1"
/db_xref="GI:32478809"
/translation="MPSKNGRSQPQPHKRWFLNNPSDERKKIRDLPISLFDYFI
VGEENEGRTPHLQGFANFVKQTFNKRWYLGARCHIEKAKGTDOONKEYCSKEGN
LLMECGAPRSQGRSDLSSTVLLSGSLVVAEHPVTFVRNFRGLLELLKRVSGM
QRDKNTNHHVIGPQCGKSKAANFADPETTKPPKRWKMDVGHGEEVVIDDFY
GKLWDDLLRLCDRVPILTVEKGTVPFLARSILITSNQPLEWYSSTAVPAVEALYR
RITSVFNKNAQESTEGGQFVTLSPCPPEFPEYNY"
complement (1033..1734)
/codon_start=1
/product="capsid"
/protein_id="AAP83628.1"
/db_xref="GI:32478810"
/translation="MTVPRRVRRRHPRSHLGOILRRRPLVHPRRHVRWRKNGI
FNRLSRFTGTRIKRTVTKTSPWAVDMRNINDFLPGGSGNSRSPFPEYRIRKVK
VEFWPCSPITGDGRGVSSAVLIDDNFVKATALTYDYNVSRHHTIQPFVSHRY
FTPFVLDSTIDYFQPNKRNQLWLRLQTAGNVHVLGTAFENSIVDQEYNIRVTY
VQRFENLKDPLNP"
CDS
ORIGIN
Query Match 99.2%; Score 1752.6; DB 14; Length 1767;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1758; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ACCGCGCATTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60
DB 1 ACCGCGCATTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60
QY 61 AGAAGATGGAAGAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCTGAATAATC 120
DB 61 AGAAGATGGAAGAGAGCGGACCCCAACCCCAATAAAGGTGGGTCTCTGAATAATC 120
QY 121 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCCAATATCCCTATTTGATATTTTA 180
DB 121 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCCAATATCCCTATTTGATATTTTA 180
QY 181 TTGTTGGCGAGGAGGTATAGGAGGACGAAACACCTCACCTCCAGGGGTTTCGCTAATT 240
DB 181 TTGTTGGCGAGGAGGTATAGGAGGACGAAACACCTCACCTCCAGGGGTTTCGCTAATT 240
QY 241 TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGGTATTTGGTGCCCGCTGCCCATCG 300
DB 241 TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGGTATTTGGTGCCCGCTGCCCATCG 300
QY 301 AGAAGCGAAGGACAGATCAGCAATAAAGATCTGCAGTAAAGAGCAACTTAC 360
DB 301 AGAAGCGAAGGACAGATCAGCAATAAAGATCTGCAGTAAAGAGCAACTTAC 360

```

```

QY 361 TGATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTACCTGTCTACTGTGTA 420
DB 361 TGATGAGTGTGGAGCTCTAGATCTCAGGGAACAAGGAGTACCTGTCTACTGTGTA 420
QY 421 GTACCTTGTGTGAGAGCGGAGTCTGGTACCGTTCAGAGCAGCAGCACCCTGTAAACGTTTG 480
DB 421 GTACCTTGTGTGAGAGCGGAGTCTGGTACCGTTCAGAGCAGCAGCACCCTGTAAACGTTTG 480
QY 481 TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGTAGCGGGAATAATGCAGAACGCTG 540
DB 481 TCAGAAATTTCCGCGGCTGGCTGAACCTTTTGAAGTGTAGCGGGAATAATGCAGAACGCTG 540
QY 541 ATTGGAAGACTAATGTACACGTCATTTGGGGCCACCTGGGTGTGTGTAAGCAAAATGGG 600
DB 541 ATTGGAAGACTAATGTACACGTCATTTGGGGCCACCTGGGTGTGTGTAAGCAAAATGGG 600
QY 601 CTGCTAATTTTCAGACCCGGAACCCACATCTTGGAAACACCTAGAAAACAAGTGTGGG 660
DB 601 CTGCTAATTTTCAGACCCGGAACCCACATCTTGGAAACACCTAGAAAACAAGTGTGGG 660
QY 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATTGATGACTTTTATGCTGGCTGGCTCCCTGGG 720
DB 661 ATGGTTACCATGGTGAAGAGTGGTTGTTATTGATGACTTTTATGCTGGCTGGCTCCCTGGG 720
QY 721 ATGATCTACGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAGGTGGAACCTG 780
DB 721 ATGATCTACGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAGGTGGAACCTG 780
QY 781 TACCTTTTGGCCCGCAGTATTCTCATATACAGCAATCAGACCCCGTTGGAAATGGTACT 840
DB 781 TACCTTTTGGCCCGCAGTATTCTCATATACAGCAATCAGACCCCGTTGGAAATGGTACT 840
QY 841 CCTCAACTGCTGTCGCCAGCTGTAGAAGTCTTTTATCGGAGTATTCTCTCGGTATTTT 900
DB 841 CCTCAACTGCTGTCGCCAGCTGTAGAAGTCTTTTATCGGAGTATTCTCTCGGTATTTT 900
QY 901 GGAAGATGCTACAGAACATCCACGGAAGAGGGGCGGAGTTCGTCAACCTTTTCCCCC 960
DB 901 GGAAGATGCTACAGAACATCCACGGAAGAGGGGCGGAGTTCGTCAACCTTTTCCCCC 960
QY 961 CATGCCCTGAAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 961 CATGCCCTGAAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 TTTTATTATTATTAAAGGTTAAGTGGGGGTCTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1080
DB 1021 TTTTATTATTATTAAAGGTTAAGTGGGGGTCTTTAAAGTAAATTAATTAATTAATTAATTAATTAAT 1080
QY 1081 ATACATGTTTACAGGATATTGTTTCCGTGCTATATATCTGTTTTCGAAACGAGTGCC 1140
DB 1081 ATACATGTTTACAGGATATTGTTTCCGTGCTATATATCTGTTTTCGAAACGAGTGCC 1140
QY 1141 GAGGCTTACGTGGTCTACATTTCCAGCAGTGTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200
DB 1141 GAGGCTTACGTGGTCTACATTTCCAGCAGTGTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200
QY 1201 GTTCTTTGTTGGAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACCG 1260
DB 1201 GTTCTTTGTTGGAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACCG 1260
QY 1261 GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1261 GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1320
QY 1321 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTATATCATCTAAATAACAGCACTGGAGCC 1380
DB 1321 ATAGGTGAGGCTGTGGCTTTTGTACAAAGTATATCATCTAAATAACAGCACTGGAGCC 1380
QY 1381 CACTCCCCTGTCAACCTGGGTGATCGGGAGCAGGGCCAGAAATTCACACCTTTAACTTCT 1440
DB 1381 CACTCCCCTGTCAACCTGGGTGATCGGGAGCAGGGCCAGAAATTCACACCTTTAACTTCT 1440
QY 1441 TATTCTGTAGTATTTCAGAGGCGCAGAGCGGGGTTTGAACCCCTCTCTCGGGGAAGAAA 1500

```



Db	1441	TATTTCTGTAGTATTTCAAAGGGCAGACAGCGGGGGTGTGAGCCCCCTCTCTGGGGGAAGAA	1500
Qy	1501	GTCAATTAATTAATTAATCTCATCATGTCCACCGCCAGGAGGGCGTTCTGACTGTGTGTCG	1560
Db	1501	GTCAATTAATTAATTAATCTCATCATGTCCACCGCCAGGAGGGCGTTCTGACTGTGTGTCG	1560
Qy	1561	CTTGACAGTATATCCGAAGTGCAGGAGCGGGTGTGAAGATGCCATTTTTCCTTCT	1620
Db	1561	CTTGATAGTATATCCGAAGTGCAGGAGCGGGTGTGAAGATGCCATTTTTCCTTCT	1620
Qy	1621	CCAGCGGTAAACGTTGCGGGGTGGACGACGAGCGCGCGCGGAGGATCTGGGCCAAG	1680
Db	1621	CCAGCGGTAAACGTTGCGGGGTGGACGACGAGCGCGCGCGGAGGATCTGGGCCAAG	1680
Qy	1681	ATGGCTGCGGGGGCGGTCTCTCTTCGGTAAACGCTCTCTTGGATACGTCAATCTCTGA	1740
Db	1681	ATGGCTGCGGGGGCGGTCTCTCTTCGGTAAACGCTCTCTTGGATACGTCAATCTCTGA	1740
Qy	1741	AAACGAAGAAGTGCCTGTAAAGTATT	1767
Db	1741	AAACGAAGAAGTGCCTGTAAAGTATT	1767
RESULT 12			
AY188355		1767 bp	DNA
LOCUS			
DEFINITION			Porcine circovirus type 2 strain HZ0201, complete genome.
ACCESSION			AY188355
VERSION			AY188355.1
KEYWORDS			GI:28396146
SOURCE			Porcine circovirus 2
ORGANISM			Porcine circovirus 2
REFERENCE			Viruses; ssDNA viruses; Circoviridae; Circovirus.
AUTHORS			1 (bases 1 to 1767)
			Zhou,J.Y., Chen,Q.X., Ye,J.X., Chen,W.J., Chen,J.G., Cheng,L.O. and Shang,S.B.
TITLE			Complete genome of HZ0201 strain of PCV-2 isolated from sows with various clinical syndromes
JOURNAL			Unpublished
REFERENCE			2 (bases 1 to 1767)
AUTHORS			Zhou,J.Y., Chen,Q.X., Ye,J.X., Chen,W.J., Chen,J.G., Cheng,L.O. and Shang,S.B.
TITLE			Direct Submision
JOURNAL			Submitted (26-NOV-2002) Institute of Preventive Veterinary Medicine, Zhejiang University, 268 Kaixuan Road, Hangzhou, Zhejiang 310029, P.R.China
FEATURES			Location/Qualifiers
source			1..1767
			/organism="Porcine circovirus 2"
			/mol_type="genomic DNA"
			/strain="HZ0201"
			/specific_host="pig"
			/db_xref="taxon:85708"
			/country="China: Zhejiang"
			/note="genotype: PCV-2"
			51..995
			/gene="rep"
gene			51..995
CDS			51..995
			/gene="rep"
			/codon_start=1
			/product="replicase"
			/protein_id="AAO39760.1"
			/db_xref="GI:28396148"
			/translation="MPSKNGRSQPHKRWVFTLNPSPDEKIKINDLPISLFDYFI VGEENEGRTPLHQLFANFVKKQTFNKKWYLGRCHIEKAGTDOONKEYCSKEG LLMCEGRPSQSDSLSTAVSLSGSLVTVAEQHPVTFVRNFRGLLELLKVSQGR KRWKNTNHHVIGPVGCGSKWAANFADPTTYWKPGRNKWMDGYHGEVWVDDPY GWLPNDLLRLCLDRYVPLTVETKGGTVPLAFLSILITSNQTPLEWYSSTAVPAVEALYR RITSLVFWKNAEQSTEGGQFVTLSPPCPEFFYIN"
gene			complement (1033..1734)
CDS			/gene="cap"
			complement (1033..1734)

```
Qy 841 CCTCAACTGCTGCTCCAGCTGTAGAACTCTTTATCGAGGATTACTTCTCGTATTTT 900
Db 841 CCTCAACTGCTGCTCCAGCTGTAGAACTCTTTATCGAGGATTACTTCTCGTATTTT 900
Qy 901 GGAAGAATGCTACAGAAATCCACGAGGAGGGGCCAGTTCGTCAACCTTTTCCCCCC 960
Db 901 GGAAGAATGCTACAGAAATCCACGAGGAGGGGCCAGTTCGTCAACCTTTTCCCCCC 960
Qy 961 CATGCCCTGAATTTCCATATGAATAAATACTAGTCTTTTTTATCATCTCGTAATGTT 1020
Db 961 CATGCCCTGAATTTCCATATGAATAAATACTAGTCTTTTTTATCATCTCGTAATGTT 1020
Qy 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGCTCTTAAATTAATCTCTGAATTCATC 1080
Db 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGCTCTTAAATTAATCTCTGAATTCATC 1080
Qy 1081 ATACATGTTTACAGGATATTTATCTCTGTCGTATATCTGTTTTCGAACGAGTGCC 1140
Db 1081 ATACATGTTTACAGGATATTTATCTCTGTCGTATATCTGTTTTCGAACGAGTGCC 1140
Qy 1141 GAGCCTACGTTGCTTACATTTCCAGCAGTTTGTAGTCTAGCCACAGCTGTTCTTTT 1200
Db 1141 GAGCCTACGTTGCTTACATTTCCAGCAGTTTGTAGTCTAGCCACAGCTGTTCTTTT 1200
Qy 1201 GTTGTGTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
Db 1201 GTTGTGTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
Qy 1261 GGAGTGTGAGGAGGCTGGGTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320
Db 1261 GGAGTGTGAGGAGGCTGGGTTATGTTATGCGGAGGAGTAGTTTACATAGGGGTC 1320
Qy 1321 ATAGTGAGGCTGTGGCTTTGTTACAAAGTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1321 ATAGTGAGGCTGTGGCTTTGTTACAAAGTATCATCTAAATAACAGCACTGGAGCC 1380
Qy 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTCT 1440
Db 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTCT 1440
Qy 1441 TATTCTGTAGTATTCAAAGGCGACAGCGGGGTTTCAACCCCTCTCGGGGGAAGAA 1500
Db 1441 TATTCTGTAGTATTCAAAGGCGACAGCGGGGTTTCAACCCCTCTCGGGGGAAGAA 1500
Qy 1501 GTCAATTAATATTAATCTCATATGTCACCGCCAGAGGGCGTTCTGACTGTGTTCTG 1560
Db 1501 GTCAATTAATATTAATCTCATATGTCACCGCCAGAGGGCGTTCTGACTGTGTTCTG 1560
Qy 1561 CTTGACAGTATATCCGAGGTCGCGAGAGGGCGGTGTTGAAGATGCCATTTTCTCTTCT 1620
Db 1561 CTTGACAGTATATCCGAGGTCGCGAGAGGGCGGTGTTGAAGATGCCATTTTCTCTTCT 1620
Qy 1621 CCAGCGGTAAACGTTGCGGGGTGACAGCAGCGGGGCGCGCGGAGGATCTGGCCCAAG 1680
Db 1621 CCAGCGGTAAACGTTGCGGGGTGACAGCAGCGGGGCGCGCGGAGGATCTGGCCCAAG 1680
Qy 1681 ATGGCTGCGGGGCGGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
Db 1681 ATGGCTGCGGGGCGGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
Qy 1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767
Db 1741 AAACGAAAGAGTGCCTCTGAAGTATT 1767
```

```
RESULT 13
AV217743
LOCUS Porcine circovirus type 2 strain HZ0202, complete genome.
DEFINITION Porcine circovirus type 2 strain HZ0202, complete genome.
ACCESSION AY217743
VERSION AY217743.1 GI:28932891
KEYWORDS Porcine circovirus 2
```

ORGANISM  
Porcine circovirus 2  
Viruses; ssDNA viruses; Circoviridae; Circovirus.  
REFERENCE  
1. (bases 1 to 1767)  
AUTHORS Zhou, J.Y., Chen, Q.X., Ye, J.X., Wang, J.Y., Chen, J.G., Chen, W.J. and Zheng, X.J.  
TITLE Complete genome of PCV-2 strain HZ0202 isolated from sows with various clinical syndrome  
JOURNAL Unpublished  
REFERENCE  
2. (bases 1 to 1767)  
AUTHORS Zhou, J.Y., Chen, Q.X., Ye, J.X., Wang, J.Y., Chen, J.G., Chen, W.J. and Zheng, X.J.  
TITLE Direct Submission  
JOURNAL Submitted (13-JAN-2003) Zhejiang University, Institute of Preventive Veterinary Medicine, 268 Kaixuan Road, Hangzhou, Zhejiang 310029, P.R. China

FEATURES  
Location/Qualifiers

source  
1. .1767  
/organism="Porcine circovirus 2"

1. .1767  
/mol\_type="genomic DNA"

1. .1767  
/strain="HZ0202"

1. .1767  
/specific\_host="pig"

1. .1767  
/db\_xref="taxon:85708"

1. .1767  
/country="China: Zhejiang"

1. .1767  
/notes="genotype: PCV-2"

1. .1767  
/gene="rep"

1. .1767  
/gene="rep"

1. .1767  
/notes="ORF1"

1. .1767  
/codon\_start=1

1. .1767  
/product="replicase protein"

1. .1767  
/protein\_id="AA061136.1"

1. .1767  
/db\_xref="GI:28932892"

1. .1767  
/translation="WPSKNGRSGQPQHKRWFTLNNPSEDERKKIRDLPLISLDFYFV  
VGESEGRKTHLQGFANFVKQFENKWLGAECHEKAGTDDQNKCYCKEEN  
LMCEGAPRSQGRSLSLSTAVSLTSSGLVTAEGHPVTFVNRFLGAEKLVSKGM  
QKRDWNTVHVIVPGPCGSKWAANFADPETTYKPPRNKWDGTHGSEVVVDYF  
GMLPMDLLRLCDRYPLTVETGGTVFPLARSILITSNQTPLEWYSSTAVPAVEALYR  
RITSLVFNKNATEQSTEGGQFVTLSPPCPEPFYEINY"

1. .1767  
/complement(1033..1734)

1. .1767  
/gene="cap"

1. .1767  
/complement(1033..1734)

1. .1767  
/gene="cap"

1. .1767  
/notes="ORF2"

1. .1767  
/codon\_start=1

1. .1767  
/product="capsid protein"

1. .1767  
/protein\_id="AA061137.1"

1. .1767  
/db\_xref="GI:28932893"

1. .1767  
/translation="MTYPRRRYRRRRRPRSHLQILRRRPLVHRRHYRWRKNGI  
FNRLSRFTGYTIKRTVTKTPSWAVDMRPNINDFLPPGGSNRSPVFPFYRIRKVK  
VEFWPCSPITQGDGSGSAVILDDNFVTKATALTALYDPPVYNSRHTITOPFYSBRY  
FTPKPLVLDSTIDYFQPNKRNQLWLRLQTAGNVHDVHGLGTAFENSIVDOEYNIRVTMY  
VQPRENLKDPPLNP"

1. .1767  
/complement(1033..1734)

1. .1767  
/gene="cap"

1. .1767  
/complement(1033..1734)

1. .1767  
/gene="cap"

1. .1767  
/notes="ORF2"

1. .1767  
/codon\_start=1

1. .1767  
/product="capsid protein"

1. .1767  
/protein\_id="AA061137.1"

1. .1767  
/db\_xref="GI:28932893"

1. .1767  
/translation="MTYPRRRYRRRRRPRSHLQILRRRPLVHRRHYRWRKNGI  
FNRLSRFTGYTIKRTVTKTPSWAVDMRPNINDFLPPGGSNRSPVFPFYRIRKVK  
VEFWPCSPITQGDGSGSAVILDDNFVTKATALTALYDPPVYNSRHTITOPFYSBRY  
FTPKPLVLDSTIDYFQPNKRNQLWLRLQTAGNVHDVHGLGTAFENSIVDOEYNIRVTMY  
VQPRENLKDPPLNP"

ORIGIN

Query Match 99.1%; Score 1751; DB 14; Length 1767;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1757; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```
Qy 1 ACCAGCGCATTCTCGGAGCGGCGAGCACCTCGGAGCACCTCAGCAGCAACATGCCAGCA 60
Db 1 ACCAGCGCATTCTCGGAGCGGCGAGCACCTCGGAGCACCTCAGCAGCAACATGCCAGCA 60
Qy 61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGTGTTCCTCTGTAATATC 120
Db 61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGTGTTCCTCTGTAATATC 120
Qy 121 CTTCCGAGAGCGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
Db 121 CTTCCGAGAGCGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 180
Qy 181 TTGTTGGCGAGGGGTAATGAGGAGGACGAAACACCTCCACCTCCAGGGGTTCGTAATT 240
```

181	Db	 TTGTGTCGAGGAGGGTAATAGAGAAAGCGAACACCTCACCTCCAGAGGGTTCGCTAAATT	240
241	Qy	 TTGTGAAGAGCAGACCTTTTAAATAAAGTGAAGTGGTATTTTGGGTGCCCGCTGCCACATCG	300
241	Db	 TTGTGAAGAAGCAGACCTTTTAAATAAAGTGAAGTGGTATTTTGGGTGCCCGCTGCCACATCG	300
301	Qy	 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATACCTGCAGTAAAGAGGCAACTTAC	360
301	Db	 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATACCTGCAGTAAAGAGGCAACTTAC	360
361	Qy	 TGATGGAGTGTGAGATCTTAGATCTCAGGGACAAAGGAGTGACCTGTCTACTGCTGTGA	420
361	Db	 TGATGGAGTGTGAGATCTTAGATCTCAGGGACAAAGGAGTGACCTGTCTACTGCTGTGA	420
421	Qy	 GTACCTTTGTTGGAGAGCGGGAGTCTGTGTACCGTTGCAGAGCAGCACCTGTAAACGTTTG	480
421	Db	 GTACCTTTGTTGGAGAGCGGGAGTCTGTGTACCGTTGCAGAGCAGCACCTGTAAACGTTTG	480
481	Qy	 TCGAAATTTCCGCGGCTGGCTGAACTTTGAAAGTGAAGCGGGAATAATCGAAGACGCTG	540
481	Db	 TCGAAATTTCCGCGGCTGGCTGAACTTTGAAAGTGAAGCGGGAATAATCGAAGACGCTG	540
541	Qy	 ATTGGAAGACTAATGTACAGTCATTTGTGGGGCCACCTGGGTGTGTAAAGCAAAATGGG	600
541	Db	 ATTGGAAGACTAATGTACAGTCATTTGTGGGGCCACCTGGGTGTGTAAAGCAAAATGGG	600
601	Qy	 CTGCTAATTTGCAGACCGGAAACCACTACTCGGAACCACTAGAAACAAGTGTGGTGGG	660
601	Db	 CTGCTAATTTGCAGACCGGAAACCACTACTCGGAACCACTAGAAACAAGTGTGGTGGG	660
661	Qy	 ATGGTTACCATGGTGAAGAAAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
661	Db	 ATGGTTACCATGGTGAAGAAAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
721	Qy	 ATGATCTACTGAGACTGTGTATCGATATCAATGACTGTAGAGACTAAAGGTGGAACCTG	780
721	Db	 ATGATCTACTGAGACTGTGTATCGATATCAATGACTGTAGAGACTAAAGGTGGAACCTG	780
781	Qy	 TACCTTTTGGCCCGCAGTATTCGTGATTACCAAGCAATCAGACCCGTTGGAATGGTACT	840
781	Db	 TACCTTTTGGCCCGCAGTATTCGTGATTACCAAGCAATCAGACCCGTTGGAATGGTACT	840
841	Qy	 CCTCAACTGTCTGCCAGCTGTAGAAGCTCTTTATCGAGGATTTACTTCCTCTGGTATTTT	900
841	Db	 CCTCAACTGTCTGCCAGCTGTAGAAGCTCTTTATCGAGGATTTACTTCCTCTGGTATTTT	900
901	Qy	 GGAAAGATGCTACAGAAACAATCCACGAGGAAGGGGCCAGTTGCTCACCTTTCCCGCCC	960
901	Db	 GGAAAGATGCTACAGAAACAATCCACGAGGAAGGGGCCAGTTGCTCACCTTTCCCGCCC	960
961	Qy	 CATGCCCTGAATTTCCATATGAATAAATTTACTGAGTCTTTTTTATCAGCTTCGTAAATGGT	1020
961	Db	 CATGCCCTGAATTTCCATATGAATAAATTTACTGAGTCTTTTTTATCAGCTTCGTAAATGGT	1020
1021	Qy	 TTTTTATTATTCATTTAAGGGTTAAGTGGGGGTCTTTTAAATTTAAATTTCTCTGAATGTAC	1080
1021	Db	 TTTTTATTATTCATTTAAGGGTTAAGTGGGGGTCTTTAAGATTAAATTTCTCTGAATGTAC	1080
1081	Qy	 ATACATGGTTACACGGATATTGTAATCTCTGGTCTGTATATCTGTTTTCGAACCGAGTCC	1140
1081	Db	 ATACATGGTTACACGGATATTGTAATCTCTGGTCTGTATATCTGTTTTCGAACCGAGTCC	1140
1141	Qy	 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT	1200
1141	Db	 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT	1200
1201	Qy	 GTTGTTGGTGGGAAGTAATCAATAGTGAATCTTAGGACAGGTTTGGGGTAAAGTACCG	1260
1201	Db	 GTTGTTGGTGGGAAGTAATCAATAGTGAATCTTAGGACAGGTTTGGGGTAAAGTACCG	1260
1261	Qy	 GGAGTGTGAGGAAGGCGCTGGGTTATGGTATGGCGGAGAGTAGTTTATACATAGGGGTC	1320

Db	1261	GGAGTGTGAGAGAGGGCTGGGTATATGTATGCGCGGAGGAGTAGTATTTACATAGGGTC	1320
Qy	1321	ATAGGTGAGGGCTGTGSCCTTTGTTTAAAGTTATCATCTAAATTAACAGCACTGAGACC	1380
Db	1321	ATAGGTGAGGGCTGTGSCCTTTGTTTAAAGTTATCATCTAGAAATAACAGCACTGGAGCC	1380
Qy	1381	CATCCCTCTGTACCCCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTAACCTTTCT	1440
Db	1381	CATCCCTCTGTACCCCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTAACCTTTCT	1440
Qy	1441	TATTCTGTAGTATTCAAAGGCGACAGAGCGGGGGTTTGACCCCTCTCGGGGGAAGAAA	1500
Db	1441	TATTCTGTAGTATTCAAAGGCGACAGAGCGGGGGTTTGACCCCTCTCGGGGGAAGAAA	1500
Qy	1501	GTCAATTAATATTGAATCTCATATGTCACCGCCAGGAGGGCTTCTGACTGTGTTCTG	1560
Db	1501	GTCAATTAATATTGAATCTCATATGTCACCGCCAGGAGGGCTTCTGACTGTGTTCTG	1560
Qy	1561	CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCCCTTCT	1620
Db	1561	CTTGATAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCCCTTCT	1620
Qy	1621	CCAGCGGTAAAGTGGCGGGGTGGACGACGACGAGGGCGCGCGGAGGATCTGGCCAAG	1680
Db	1621	CCAGCGGTAAAGTGGCGGGGTGGACGACGACGAGGGCGCGCGGAGGATCTGGCCAAG	1680
Qy	1681	ATGCTCGGGGGCGGTGTCTTCTTTCGGTAAACGCTCCTTGGATACGTATATCTGA	1740
Db	1681	ATGCTCGGGGGCGGTGTCTTCTTTCGGTAAACGCTCCTTGGATACGTATATCTGA	1740
Qy	1741	AAACGAAAGATCGCTGTAAATATT	1767
Db	1741	AAACGAAAGATCGCTGTAAATATT	1767
RESULT 14			
AV321988		1767 bp	DNA
LOCUS			circular VRL 11-FEB-2004
DEFINITION			Porcine circovirus 2 strain Fd11, complete genome.
ACCESSION			AV321988
VERSION			AV321988.1
KEYWORDS			GI:32478772
SOURCE			Porcine circovirus 2
ORGANISM			Porcine circovirus 2
REFERENCE			Viruses; ssDNA viruses; Circoviridae; Circovirus.
AUTHORS			1 (bases 1 to 1767)
			de Boissezon, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
			Eveno, E., Mader, P. and Jestin, A.
TITLE			Molecular characterization of Porcine circovirus type 2 isolates
			from post-weaning multisystemic wasting syndrome-affected and
			non-affected pigs
			J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
JOURNAL			14769887
PUBMED			2 (bases 1 to 1767)
REFERENCE			de Boissezon, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
AUTHORS			Eveno, E., Mader, P. and Jestin, A.
TITLE			Direct Submission
JOURNAL			Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
			Food safety Agency, BP 53 Ploufragan 22 440, France
FEATURES			Location/Qualifiers
source			1..1767
			/organism="Porcine circovirus 2"
			/vision
			/mol_type="genomic DNA"
			/strain="Fd11"
			/db_xref="taxon:85708"
			/note="type: 2"
			51..995
			/codon_start=1
			/product="replicase"
			/protein_id="AAP83603.1"
			/db_xref="GI:32478773"
			/translation="MPKSKNGRSGQPQHKRWVFTLNPSDEKRIIDLPLSLFDYF"
CDS			

VBEENEGRTPHLOGFANFKVQTFNFKVWYLGARCHIEKAKGTDOONKEYCSKEGN LLMECGRPSQORSLSLSTAVSLTLESGLVTVABOHPVTFVFNFRGLAELLKVSQKM QKDWKTNVHVIVGPPCGSKSNANFADRETYWKPKNKWDGVBGEVVIDDQY GMLPDDLLRLCDRIPLUTVBKGTVPFLARSILITNSQTPLEWISVAPVAEALYR RITSLVFNKATEQSTBEGQFVTLSPPCPEPPEYNY" complement (1033..1734) /codon_start=1 /product="capsid" /protein_id="AAP83604.1" /db_xref="GI:32478774" /translation="MTYPRRRYRRRRPRSHLQILRRPWLHPHRRVRRKNGI FNRLSRFTFGVTRKTVTPSPWAVDMNFRINDEFLPPGGSNPRSPVFFYYIRKYK VEFWPCSPITQDGRGVSSAVILDNFWTKATALTYPYVNYSSRHITOPFFSYHSRY FTPKPVLDSIDIVFQPNKNQNLWLRLOTAGNVHDVGLGTAFAENSIYDQEVNIRVTMY VQREFNLKDFPLNP"									
ORIGIN									
Query Match 99.1%; Score 1751; DB 14; Length 1767; Best Local Similarity 99.4%; Pred. No. 0; Matches 1757; Conservative 0; Mismatches 10; Indels 0; Gaps 0;									
Qy	1	ACCAGGCACTTCGGCAGCGGAGCCTCGGAGGACCTCAGCAGCAACATGCCAGCA	60						
Db	1	ACCAGGCACTTCGGCAGCGGAGCCTCGGAGGACCTCAGCAGCAACATGCCAGCA	60						
Qy	61	AGAGNATGGAAGAGCGGACCCCAACCCCAATAAAGTGCGTTCACCTCTGAATAATC	120						
Db	61	AGAGNATGGAAGAGCGGACCCCAACCCCAATAAAGTGCGTTCACCTCTGAATAATC	120						
Qy	121	CTTCGGAAGACGAGCGCAAGAAATACCGGATCTTCCAATATCCCTATTTGATTTTA	180						
Db	121	CTTCGGAAGACGAGCGCAAGAAATACCGGATCTTCCAATATCCCTATTTGATTTTA	180						
Qy	181	TTGTTGGCGAGGAGGTAAATGAGNAGCAACACCTCACCTCAGGGGTTCCTAATT	240						
Db	181	TTGTTGGCGAGGAGGTAAATGAGNAGCAACACCTCACCTCAGGGGTTCCTAATT	240						
Qy	241	TTGTGAAGACGACACTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG	300						
Db	241	TTGTGAAGACGACACTTTTAATAAGTGAAGTGTATTTGGTGCCCGCTGCCACATCG	300						
Qy	301	AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGCAACTTAC	360						
Db	301	AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGCAACTTAC	360						
Qy	361	TGATGGAGTGGAGCTCTAGATCTCAGGACCAACCGAGTGACCTGTCTACTGTGTA	420						
Db	361	TGATGGAGTGGAGCTCTAGATCTCAGGACCAACCGAGTGACCTGTCTACTGTGTA	420						
Qy	421	GTACCTTGTGGAGAGCGGAGTCTGTGTGACCGTTGCAGAGCAGCACCTGTACGTTG	480						
Db	421	GTACCTTGTGGAGAGCGGAGTCTGTGTGACCGTTGCAGAGCAGCACCTGTACGTTG	480						
Qy	481	TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATGAGAAAGCGTG	540						
Db	481	TCAGAAATTTCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATGAGAAAGCGTG	540						
Qy	541	ATTGGAAGACTAATGTACACGTCACTGTGGGCGCACCTGGGTGTGTTAAAGCAATGGG	600						
Db	541	ATTGGAAGACTAATGTACACGTCACTGTGGGCGCACCTGGGTGTGTTAAAGCAATGGG	600						
Qy	601	CTGCTAATTTTCAGACCCGGAACCAACATCTCGAAACCACTAGAAACCAAGTGGTGGG	660						
Db	601	CTGCTAATTTTCAGACCCGGAACCAACATCTCGAAACCACTAGAAACCAAGTGGTGGG	660						
Qy	661	ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG	720						
Db	661	ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG	720						
Qy	721	ATGATCTACTGAGCTGTGTGATCGATATCCATTCGATCTGAGACTAAAGTGGAATCG	780						
Db	721	ATGATCTACTGAGCTGTGTGATCGATATCCATTCGATCTGAGACTAAAGTGGAATCG	780						

RESULT 15  
AV321990  
LOCUS  
DEFINITION Porcine circovirus 2 strain Fd7, complete genome.

1767 bp DNA circular VRL 11-FEB-2004

Qy	781	TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT	840
Db	781	TACCTTTTGGCCCGCAGTATCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT	840
Qy	841	CCTCAACTCTGTCCCGCAGTGTAGAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT	900
Db	841	CCTCAACTCTGTCCCGCAGTGTAGAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT	900
Qy	901	GGAGAATGCTACAGAAACAATCCACGGAGGAAGGGGCCAGTTCGTCAACCTTTCCCCCC	960
Db	901	GGAGAATGCTACAGAAACAATCCACGGAGGAAGGGGCCAGTTCGTCAACCTTTCCCCCC	960
Qy	961	CATGCCCTGAATTTCCATATGAATAAATACGTAGCTCTTTTATCAGTCTGTATGGT	1020
Db	961	CATGCCCTGAATTTCCATATGAATAAATACGTAGCTCTTTTATCAGTCTGTATGGT	1020
Qy	1021	TTTTATTAATTAAGGCTTAAGTGGGGTCTTTAAATAAATTTCTCTGAATTTGTAC	1080
Db	1021	TTTTATTAATTAAGGCTTAAGTGGGGTCTTTAAATAAATTTCTCTGAATTTGTAC	1080
Qy	1081	ATACATGGTTACACGGATATTTGATTTCTCTGGTCTGTATATCTGTTTTCGAACGAGTGCC	1140
Db	1081	ATACATGGTTACACGGATATTTGATTTCTCTGGTCTGTATATCTGTTTTCGAACGAGTGCC	1140
Qy	1141	GAGGCTACGTGGTCTACATTTCCAGAGTGTGTAGTCTCAGCAGCAGCTGTTCTTTT	1200
Db	1141	GAGGCTACGTGGTCTACATTTCCAGAGTGTGTAGTCTCAGCAGCAGCTGTTCTTTT	1200
Qy	1201	GTGTTTGGTGGAGTAACTCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACCG	1260
Db	1201	GTGTTTGGTGGAGTAACTCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACCG	1260
Qy	1261	GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTTACATAGGGGTC	1320
Db	1261	GGAGTGTAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTAGTTACATAGGGGTC	1320
Qy	1321	ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGACTGGAGCC	1380
Db	1321	ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATAACAGACTGGAGCC	1380
Qy	1381	CACCTCCCTGTACCCCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTTCT	1440
Db	1381	CACCTCCCTGTACCCCTGGGTGATCGGGAGCAGGCGCAGAAATCAACCTTTAACTTTCT	1440
Qy	1441	TATTTCTAGTATTTCAAAGGGCAAGAGCGGGGTTTGAACCCCTCTCTGGGGAGAGAA	1500
Db	1441	TATTTCTAGTATTTCAAAGGGCAAGAGCGGGGTTTGAACCCCTCTCTGGGGAGAGAA	1500
Qy	1501	GTCAATTAATTTGAATCTCATCTGTCACCGCCAGGAGGGGCTCTGACTGTGGTTCG	1560
Db	1501	GTCAATTAATTTGAATCTCATCTGTCACCGCCAGGAGGGGCTCTGACTGTGGTTCG	1560
Qy	1561	CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAGATGCAATTTTCTTCT	1620
Db	1561	CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAGATGCAATTTTCTTCT	1620
Qy	1621	CCAGCGGTAAACGGTGGCGGGGTGGACAGCCAGGGCGCGCGGAGGATCTGGCCCAAG	1680
Db	1621	CCAGCGGTAAACGGTGGCGGGGTGGACAGCCAGGGCGCGCGGAGGATCTGGCCCAAG	1680
Qy	1681	ATGGCTCGGGGGGGGTGTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA	1740
Db	1681	ATGGCTCGGGGGGGGTGTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA	1740
Qy	1741	AAACGAAAGAGTGGCTGTAAAGTATT 1767	
Db	1741	AAACGAAAGAGTGGCTGTAAAGTATT 1767	

ACCESSION	AY321990	Db	241	TTGTGAAGAAGCAGACCTTTTAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG	300
VERSION	AY321990.1	Qy	301	AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATACTGCAGTAAGAAAGGCAACTTAC	360
KEYWORDS		Db	301	AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATACTGCAGTAAGAAAGGCAACTTAC	360
SOURCE	Porcine circovirus 2	Qy	361	TGATGGAGTGGAGCTCTAGATCTCAGGACAAACGGAGTGACCTGTCTACTCTGTGA	420
ORGANISM	Viruses; ssDNA viruses; Circoviridae; Circovirus.	Db	361	TGATGGAGTGGAGCTCTAGATCTCAGGACAAACGGAGTGACCTGTCTACTCTGTGA	420
REFERENCE	1 (bases 1 to 1767)	Qy	421	GTACCTTTGTCGAGCGGGAGTCTGGTGACCGTTTGACAGACAGCACCCTCTGAACGTTTG	480
AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.	Db	421	GTACCTTTGTCGAGCGGGAGTCTGGTGACCGTTTGACAGACAGCACCCTCTGAACGTTTG	480
TITLE	Molecular characterization of Porcine circovirus type 2 isolates from post-weaning multisystemic wasting syndrome-affected and non-affected pigs	Qy	481	TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAATAACAGAACGCTG	540
JOURNAL	J. Gen. Virol. 85 (Pt 2), 293-304 (2004)	Db	481	TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGTGAGCGGGAATAACAGAACGCTG	540
PUBMED	14769887	Qy	541	ATTGGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAATGGG	600
REFERENCE	2 (bases 1 to 1767)	Db	541	ATTGGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAATGGG	600
AUTHORS	de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Eveno,E., Madec,F. and Jestin,A.	Qy	601	CTGCTAATTTTGCAGACCCGGAACCACTACTTGAACACCACTTGAAGCTGAAGCTGGA	660
TITLE	Direct Submission	Db	601	CTGCTAATTTTGCAGACCCGGAACCACTACTTGAACACCACTTGAAGCTGAAGCTGGA	660
JOURNAL	Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French Food Safety Agency, BP 53, Ploufragan 22 440, France	Qy	661	ATGTTTACCATGTGCAAGAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGG	720
FEATURES	Location/Qualifiers	Db	661	ATGTTTACCATGTGCAAGAGTGGTTGTTATTTGATGACTTTTATGGCTGGCTGCCCTGG	720
source	1. 1767 /organism="Porcine circovirus 2"	Qy	721	ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGGTGAACCTG	780
	/vision	Db	721	ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGGTGAACCTG	780
	/mol_type="genomic DNA"	Qy	781	TACCTTTTTCGCGCGAGTATCTGATTACCAGCAATCAGACCCGCTTGGAAATGGTACT	840
	/strain="Fd7"	Db	781	TACCTTTTTCGCGCGAGTATCTGATTACCAGCAATCAGACCCGCTTGGAAATGGTACT	840
	/db_xref="taxon:85708"	Qy	841	CCTCAACTGCTGTCCAGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT	900
	/note="type: 2"	Db	841	CCTCAACTGCTGTCCAGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTCTCTGGTATTTT	900
	51. .995 /codon_start=1	Qy	901	GGAAGAAATGCTACAGAAACAATCCAGGAGGAAGGGGGCAGTTCGTACCCCTTCCCGCC	960
	/product="replicase"	Db	901	GGAAGAAATGCTACAGAAACAATCCAGGAGGAAGGGGGCAGTTCGTACCCCTTCCCGCC	960
	/protein_id="AAP83607.1"	Qy	961	CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGCT	1020
	/db_xref="GI:3247879"	Db	961	CATGCCCTGAATTTCCATATGAATAAATTAATCTGAGTCTTTTATCACTTCGTAATGCT	1020
	/translation="MPSKNGRSQPHKRWFTLNPSDEKRIKIDLPISLDFYI VBEGBEGRPHLGDFANFKVTKWTLGARCHIEKAKGTDQNKKEYCSKEGN LMECGASQGRDLSLSTVSLSESLVTPAOPVTFVFRNFRGAEILLKVSCKM OKRDWTVHVIQVPGGCKGKAANFADPETTYWKPKNKWDVHGHEVVVDDFY GWLWDLLRLCDRPLVETGKGVPLFARSLITSNQTPLEWYSSTAVPAVEALYR RITSLVFWKNATQSTEGSQVTLSPCPPEFYIN"	Qy	1021	TTTTTATTTCATTAAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGTAC	1080
	complement(1033..1734)	Db	1021	TTTTTATTTCATTAAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGTAC	1080
	/codon_start=1	Qy	1081	ATACATGTTTACACGGATATTGTAATCTCTGGTGGTATATCTGTTTTTGAACGCGAGTGC	1140
	/product="capsid"	Db	1081	ATACATGTTTACACGGATATTGTAATCTCTGGTGGTATATCTGTTTTTGAACGCGAGTGC	1140
	/protein_id="AAP83608.1"	Qy	1141	GAGGCTACGTGCTCTACATTTCCAGCAGTTTGTAGTCTCAGGCCACAGCTGGTTCCTTTT	1200
	/db_xref="GI:3247878"	Db	1141	GAGGCTACGTGCTCTACATTTCCAGCAGTTTGTAGTCTCAGGCCACAGCTGGTTCCTTTT	1200
	/translation="WTYPRRYRRHPRSHLGOILRRPWLHPHRYRWRKNGI FNTRSRFTGYTKRTTWTKPSWADMMRFNIDLPFGGSGNPRSPVFYRIRKVK VEFWPCSPITQGRDVGSSAVILDNFTVKATLTDYVNYSSRHTITQPPYSHSRY FTPKPLDSTIDYFQPNKRNQLRLQTAGNVHVLGTAFENSIDYQEVNIRVTMY VQFRFNLKDPPLNP"	Qy	1201	GTGTTTGTGTCGAAGTAAATCAATAGTGAATCTTAGGACAGGTTTGGGGGTAAAGTACCG	1260
		Db	1201	GTGTTTGTGTCGAAGTAAATCAATAGTGAATCTTAGGACAGGTTTGGGGGTAAAGTACCG	1260
		Qy	1261	GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGAGGAGTAGTTCATACATAGGGGTC	1320
		Db	1261	GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGAGGAGTAGTTCATACATAGGGGTC	1320
		Qy	1321	ATAGGTGAGGGCTGTGGCCCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC	1380
		Db	1321	ATAGGTGAGGGCTGTGGCCCTTTGTTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC	1380
ORIGIN	Query Match 99.1%; Score 1751; DB 14; Length 1767; Best Local Similarity 99.4%; Pred. No. 0; Matches 1757; Conservative 0; Mismatches 10; Indels 0; Gaps 0;				
Qy	1 ACCAGGCACTTCGGCAGCGGAGCAGCTCGGAGCAGCTCAGCAGCAATGCCAGCA 60				
Db	1 ACCAGGCACTTCGGCAGCGGAGCAGCTCGGAGCAGCTCAGCAGCAATGCCAGCA 60				
Qy	61 AGAAGAAATGGAAGAGCGGACCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 120				
Db	61 AGAAGAAATGGAAGAGCGGACCCCAACCCCATAAAGTGGGTGTTCACTCTGAATAATC 120				
Qy	121 CTTCCGAGACGAGCCAGAAATAACGGGATCTTCCAATATCCCTATTGATATTATTA 180				
Db	121 CTTCCGAGACGAGCCAGAAATAACGGGATCTTCCAATATCCCTATTGATATTATTA 180				
Qy	181 TTGTTGGCAGGAGGATATGAGGAGGAGGACACCTCACCTCCAGGGGTTCGCTAATT 240				
Db	181 TTGTTGGCAGGAGGATATGAGGAGGAGGACACCTCACCTCCAGGGGTTCGCTAATT 240				
Qy	241 TTGTGAAGAAGCAGACCTTTTAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300				

```
Qy 1381 CACTCCCTGTACCTGGGTGATCGGGAGCGGGCCAGAAATTCACCTTTAACTTTCT 1440
Db 1381 CACTCCCTGTACCTGGGTGATCGGGAGCGGGCCAGAAATTCACCTTTAACTTTCT 1440
Qy 1441 TATTCTGTAGTATTCAAAGGSCACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAA 1500
Db 1441 TATTCTGTAGTATTCAAAGGSCACAGAGCGGGGTTTGAGCCCCCTCTCTGGGGGAAGAA 1500
Qy 1501 GTCATTAAATTTGAATCTCATCTGTCACCGCCAGAGGGCGTTCTGACTGTGGTTCG 1560
Db 1501 GTCATTAAATTTGAATCTCATCTGTCACCGCCAGAGGGCGTTTGAATGTGGTTCG 1560
Qy 1561 CTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTCT 1620
Db 1561 CTTGATAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCTCTCT 1620
Qy 1621 CCAGCGGTAAACGGTGGCGGGGTGGACGAGCCAGGGCGCGGAGGATCTGCCCAAG 1680
Db 1621 CCAGCGGTAAACGGTGGCGGGGTGGACGAGCCAGGGCGCGGAGGATCTGCCCAAG 1680
Qy 1681 ATGGCTCGGGGGCGGTGTCTTCTTTCGGTAACGGCTCCTTGGATACGTATATCTGA 1740
Db 1681 ATGGCTCGGGGGCGGTGTCTTCTTTCGGTAACGGCTCCTTGGATACGTATATCTGA 1740
Qy 1741 AAACGAAGAAGTGGCTGTAAATTT 1767
Db 1741 AAACGAAGAAGTGGCTGTAAATTT 1767
```

Search completed: December 7, 2004, 20:03:01  
Job time : 7544 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:40:24 ; Search time 158 Seconds  
(without alignments)  
7949.139 Million cell updates/sec

Title: US-10-718-264-15  
Perfect score: 1767  
Sequence: 1 accagcgacttcggcagc.....agaagtgcgtgaagtatt 1767

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/5A COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1767	100.0	1767	4	US-09-514-245-15
2	1767	100.0	1767	4	US-09-514-245-19
3	1642.4	92.9	1768	4	US-09-583-350-8
4	1636.8	92.6	1768	4	US-09-583-350-7
5	1620	91.7	1768	4	US-10-112-540-1
6	1412	79.9	1767	3	US-09-347-594-1
7	1412	79.9	1767	3	US-09-082-558-1
8	1412	79.9	1767	3	US-09-161-092-1
9	1412	79.9	1767	4	US-09-583-350-1
10	1412	79.9	1767	4	US-09-884-514-1
11	1410.4	79.8	1767	3	US-09-347-594-2
12	1410.4	79.8	1767	3	US-09-082-558-2
13	1410.4	79.8	1767	3	US-09-161-092-2
14	1410.4	79.8	1767	4	US-09-583-350-2
15	1410.4	79.8	1767	4	US-09-884-514-2
16	1335.4	75.6	1768	3	US-09-347-594-3
17	1335.4	75.6	1768	3	US-09-082-558-3
18	1335.4	75.6	1768	3	US-09-161-092-3
19	1335.4	75.6	1768	3	US-09-583-350-3
20	1335.4	75.6	1768	3	US-09-884-514-3
21	1335.4	75.6	1768	3	US-09-347-594-4
22	1335.4	75.6	1768	3	US-09-082-558-4
23	1335.4	75.6	1768	3	US-09-161-092-4
24	1335.4	75.6	1768	3	US-09-583-350-4
25	1335.4	75.6	1768	3	US-09-884-514-4
26	1324.6	75.0	1768	3	US-09-082-558-5
27	1324.6	75.0	1768	3	US-09-161-092-6

28	1324.6	75.0	1768	4	US-09-583-350-6
29	1324.6	75.0	1768	4	US-09-884-514-6
30	1007.2	57.0	1759	4	US-09-514-245-1
31	1005.6	56.9	1759	4	US-09-514-245-163
32	1004	56.8	1759	4	US-09-514-245-5
33	1000.8	56.6	1759	3	US-09-267-177-38
34	1000.8	56.6	1759	3	US-09-267-177-40
35	1000.8	56.6	1759	4	US-09-514-245-164
36	984.6	55.7	1727	3	US-09-267-177-2
37	970.6	54.9	1674	3	US-09-267-177-1
38	945	53.5	945	4	US-09-514-245-23
39	920.8	52.1	3609	4	US-09-583-350-13
40	886.4	50.2	1759	3	US-09-347-594-5
41	886.4	50.2	1759	3	US-09-082-558-5
42	886.4	50.2	1759	3	US-09-161-092-5
43	886.4	50.2	1759	4	US-09-583-350-5
44	886.4	50.2	1759	4	US-09-884-514-5
45	702	39.7	702	4	US-09-514-245-25

ALIGNMENTS

RESULT 1  
US-09-514-245-15  
; Sequence 15, Application US/09514245  
; Patent No. 6703023  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/09/514,245  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Type B PWD circovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(111)  
; NAME/KEY: CDS  
; LOCATION: (115)..(243)  
; NAME/KEY: CDS  
; LOCATION: (247)..(267)  
; NAME/KEY: CDS  
; LOCATION: (271)..(360)  
; NAME/KEY: CDS  
; LOCATION: (364)..(417)  
; NAME/KEY: CDS  
; LOCATION: (421)..(447)  
; NAME/KEY: CDS  
; LOCATION: (451)..(471)  
; NAME/KEY: CDS  
; LOCATION: (475)..(510)  
; NAME/KEY: CDS  
; LOCATION: (514)..(516)  
; NAME/KEY: CDS  
; LOCATION: (520)..(729)  
; NAME/KEY: CDS  
; LOCATION: (733)..(753)

Sequence 6, Appli  
Sequence 6, Appli  
Sequence 1, Appli  
Sequence 163, App  
Sequence 5, Appli  
Sequence 38, Appl  
Sequence 40, Appl  
Sequence 164, App  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 23, Appl  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 25, Appli



NAME/KEY: CDS  
LOCATION: (757) .. (759)  
NAME/KEY: CDS  
LOCATION: (763) .. (804)  
NAME/KEY: CDS  
LOCATION: (808) .. (861)  
NAME/KEY: CDS  
LOCATION: (865) .. (984)  
NAME/KEY: CDS  
LOCATION: (988) .. (1173)  
NAME/KEY: CDS  
LOCATION: (1177) .. (1233)  
NAME/KEY: CDS  
LOCATION: (1237) .. (1359)  
NAME/KEY: CDS  
LOCATION: (1363) .. (1476)  
NAME/KEY: CDS  
LOCATION: (1480) .. (1737)  
NAME/KEY: CDS  
LOCATION: (1741) .. (1767)  
US-09-514-245-15

Query Match 100.0%; Score 1767; DB 4; Length 1767;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCAGCGACATTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60  
DB 1 ACCAGCGACATTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60

QY 61 AGAAGATGGAAGACGGGACCCCAACCCCATAAAGTGGGTCTCACTCTGAATATC 120  
DB 61 AGAAGATGGAAGACGGGACCCCAACCCCATAAAGTGGGTCTCACTCTGAATATC 120

QY 121 CTTCCGAGACGAGCGCAAGAAATACGGATCTTCCAAATATCCCTATTTGATTTT 180  
DB 121 CTTCCGAGACGAGCGCAAGAAATACGGATCTTCCAAATATCCCTATTTGATTTT 180

QY 181 TTGTTGGCGAGGAGGTATAGGAAGGACGAACACCTCACCTCAGGGGTTCGTAAT 240  
DB 181 TTGTTGGCGAGGAGGTATAGGAAGGACGAACACCTCACCTCAGGGGTTCGTAAT 240

QY 241 TTGTGAGAGCAGACTTTTAAATGAAGTGAAGTGTATTTGGTCCCGCTGCCACATCG 300  
DB 241 TTGTGAGAGCAGACTTTTAAATGAAGTGAAGTGTATTTGGTCCCGCTGCCACATCG 300

QY 301 AGAAGCGAAAGCAAGATCAGCAGATTAAGAAATACCTGAGTAAAGAGCAACTTAC 360  
DB 301 AGAAGCGAAAGCAAGATCAGCAGATTAAGAAATACCTGAGTAAAGAGCAACTTAC 360

QY 361 TGATGAGGTGTGAGCTCTAGATCTCAGGACCAACGGAGTCACTGTCTACTGTGTA 420  
DB 361 TGATGAGGTGTGAGCTCTAGATCTCAGGACCAACGGAGTCACTGTCTACTGTGTA 420

QY 421 GTACCTTTGTGAGAGCGGAGTCTGTGACCTTCAGAGCAGCACCTGTAAAGTTG 480  
DB 421 GTACCTTTGTGAGAGCGGAGTCTGTGACCTTCAGAGCAGCACCTGTAAAGTTG 480

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGCGGTG 540  
DB 481 TCAGAAATTTCCCGGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATTCAGAGCGGTG 540

QY 541 ATTGGAAGACTAATGTACAGTCAATTTGTGGGCGACCTGGGTGTGTAAAGCAATGG 600  
DB 541 ATTGGAAGACTAATGTACAGTCAATTTGTGGGCGACCTGGGTGTGTAAAGCAATGG 600

QY 601 CTGCTAATTTTGAGACCCGGAACCACTACTGGAACCACTAGAAACAAGTGTGGG 660  
DB 601 CTGCTAATTTTGAGACCCGGAACCACTACTGGAACCACTAGAAACAAGTGTGGG 660

QY 661 ATGGTTACCAATGGTGAAGAGTGGTGTATGATGACTTTTATGGCTGCTGCCCTGG 720  
DB 661 ATGGTTACCAATGGTGAAGAGTGGTGTATGATGACTTTTATGGCTGCTGCCCTGG 720

QY 721 ATGATCTACTGAGACTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAC 780  
DB 721 ATGATCTACTGAGACTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAAC 780

QY 781 TACCTTTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTTGGAATGGTACT 840  
DB 781 TACCTTTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTTGGAATGGTACT 840

QY 841 CTTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTTCTGGTATTTT 900  
DB 841 CTTCAACTGTCTCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTTCTGGTATTTT 900

QY 901 GGAAGATCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTTCCCCC 960  
DB 901 GGAAGATCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCGTCAACCTTTTCCCCC 960

QY 961 CATGCCCTGAATTTCCATATGAATAAATTAAGTCTTTTTTATCATCTTCTGTAATGGT 1020  
DB 961 CATGCCCTGAATTTCCATATGAATAAATTAAGTCTTTTTTATCATCTTCTGTAATGGT 1020

QY 1021 TTTTATTTATTAAGGTTAAGTGGGGTCTTTAAATTAATTTCTCTCAATTTGATAC 1080  
DB 1021 TTTTATTTATTAAGGTTAAGTGGGGTCTTTAAATTAATTTCTCTCAATTTGATAC 1080

QY 1081 ATACATGGTTACACGGATATTTCTCTGGTCTGATATATCTTTTTCGAAACGAGTGCC 1140  
DB 1081 ATACATGGTTACACGGATATTTCTCTGGTCTGATATATCTTTTTCGAAACGAGTGCC 1140

QY 1141 GAGGCTTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTCTTTT 1200  
DB 1141 GAGGCTTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTCTTTT 1200

QY 1201 GTTGTGTTGTTGGAAGTAACTAGGACAGGTTTGGGGTAAAGTACCG 1260  
DB 1201 GTTGTGTTGTTGGAAGTAACTAGGACAGGTTTGGGGTAAAGTACCG 1260

QY 1261 GAGTGTGAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTGTATCATAGGGGTC 1320  
DB 1261 GAGTGTGAGGAGAGGGCTGGGTATGTTATGCGGGAGGAGTGTATCATAGGGGTC 1320

QY 1321 ATAGTGAGGGCTGTGGCTTTGTTTCAAGTTATCATCTAAATTAACAGCAGCTGGAGCC 1380  
DB 1321 ATAGTGAGGGCTGTGGCTTTGTTTCAAGTTATCATCTAAATTAACAGCAGCTGGAGCC 1380

QY 1381 CACTCCCTCTGACCCCTGGGTGATCGGGAGCAGGGCCAGAAATTCACCTTAACCTTTCT 1440  
DB 1381 CACTCCCTCTGACCCCTGGGTGATCGGGAGCAGGGCCAGAAATTCACCTTAACCTTTCT 1440

QY 1441 TATTCTGTAGTATTCAAGGGCAGAGCGGGGTTTGACCCCTCTGGGGAGGAA 1500  
DB 1441 TATTCTGTAGTATTCAAGGGCAGAGCGGGGTTTGACCCCTCTGGGGAGGAA 1500

QY 1501 GTCAATTAATTTGATCTCATCTCCACCGCCAGAGGGGTTCTGACTGTGGTTCG 1560  
DB 1501 GTCAATTAATTTGATCTCATCTCCACCGCCAGAGGGGTTCTGACTGTGGTTCG 1560

QY 1561 CTTGACAGTATATCCGAAAGTTCGCGGAGAGCGGGTGTGGAAGATGCCATTTTCTTCT 1620  
DB 1561 CTTGACAGTATATCCGAAAGTTCGCGGAGAGCGGGTGTGGAAGATGCCATTTTCTTCT 1620

QY 1621 CCAGCGGTAAACGGTGGCGGGGTGGACAGCCAGGGGCGGGGAGGATCTGGCCCAAG 1680  
DB 1621 CCAGCGGTAAACGGTGGCGGGGTGGACAGCCAGGGGCGGGGAGGATCTGGCCCAAG 1680

QY 1681 ATGGCTGGGGGCGGTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA 1740  
DB 1681 ATGGCTGGGGGCGGTCTTCTTCTCGGTAAACGCTCTCTTGGATACGTCATATCTGA 1740

QY 1741 AAACGAAAGAGTGGCTGTAAAGTATT 1767  
DB 1741 AAACGAAAGAGTGGCTGTAAAGTATT 1767

```
RESULT 2
US-09-514-245-19/c
; Sequence 19, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CAROLET, Roland
; APPLICANT: MADSC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Type B PWD circovirus
US-09-514-245-19

Query Match 100.0%; Score 1767; DB 4; Length 1767;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1767; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCAGCGCATTCTGGCAGCGGAGCAGCCTCGGAGCACCTCAGCAGCAACATGCCAGCA 60
DB 1767 ACCAGCGCATTCTGGCAGCGGAGCAGCCTCGGAGCACCTCAGCAGCAACATGCCAGCA 1708

QY 61 AGAAGATCGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCAGCTCGAATAATC 120
DB 1707 AGAAGATCGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCAGCTCGAATAATC 1648

QY 121 CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTAATTTA 180
DB 1647 CTTCCGAAGCAGGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTAATTTA 1588

QY 181 TTGTTGGCAGGAGGGTAAATGAGGAAGGACGAAACCTCACCTCCAGGGGTCGCTAAT 240
DB 1587 TTGTTGGCAGGAGGGTAAATGAGGAAGGACGAAACCTCACCTCCAGGGGTCGCTAAT 1528

QY 241 TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGAATTTGGGTGCCCGCTGCCACATCG 300
DB 1527 TTGTGAAGAGCAGACTTTTAATAAGTGAAGTGAATTTGGGTGCCCGCTGCCACATCG 1468

QY 301 AGAAGCGAAGGAACAGATCAGCAGATTAAGAAATACCTGCACTAAAGAGGCAACTTAC 360
DB 1467 AGAAGCGAAGGAACAGATCAGCAGATTAAGAAATACCTGCACTAAAGAGGCAACTTAC 1408

QY 361 TGATGGAGTGTGGAGTCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA 420
DB 1407 TGATGGAGTGTGGAGTCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA 1348

QY 421 GTACCTTTTGGAGAGCGGAGTCTGGTGACCGTTGAGAGCAGACCCCTGTAACTTTG 480
DB 1347 GTACCTTTTGGAGAGCGGAGTCTGGTGACCGTTGAGAGCAGACCCCTGTAACTTTG 1288

QY 481 TCAGAAATTTCCCGGCGCTGGCTGAATTTTGAAGAGTGAGCGGGAATAATGCAGAGCGTG 540
DB 1287 TCAGAAATTTCCCGGCGCTGGCTGAATTTTGAAGAGTGAGCGGGAATAATGCAGAGCGTG 1228

QY 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTAAAGCAATGGG 600
DB 1227 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACCTGGGTGTGTAAAGCAATGGG 1168
```

```
QY 601 CTGCTAAATTTTGCAGACCCCGGAAACCACTACTCGAAACCACTAGAAAAAAGTGGTGG 660
DB 1167 CTGCTAAATTTTGCAGACCCCGGAAACCACTACTCGAAACCACTAGAAAAAAGTGGTGG 1108

QY 661 ATGGTTACCATGGTGAAGAAGTGGTCTTATTTGATGACTTTTATGGCTGGCTGCCCTGG 720
DB 1107 ATGGTTACCATGGTGAAGAAGTGGTCTTATTTGATGACTTTTATGGCTGGCTGCCCTGG 1048

QY 721 ATGATCTACTGAGACTGTGATCGATATCATTTGACTGTAGAGACTAAAGGTGGAACCTG 780
DB 1047 ATGATCTACTGAGACTGTGATCGATATCATTTGACTGTAGAGACTAAAGGTGGAACCTG 988

QY 781 TACCTTTTTCGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840
DB 987 TACCTTTTTCGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 928

QY 841 CCTCAACTGCTGTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 927 CCTCAACTGCTGTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 868

QY 901 GGAAGATGCTACAGAACAAATCCACGAGAGGAGGGGCCAGTTCGTCAACCTTTCCGCC 960
DB 867 GGAAGATGCTACAGAACAAATCCACGAGAGGAGGGGCCAGTTCGTCAACCTTTCCGCC 808

QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCGTAAATGGT 1020
DB 807 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCGTAAATGGT 748

QY 1021 TTTTATTAATCAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATCTCTGAATTTG 1080
DB 747 TTTTATTAATCAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATCTCTGAATTTG 688

QY 1081 ATACATGTTTACACCGATATTTGATTTCTGTCGCTATATCTACTGTTTTCGAAAGCG 1140
DB 687 ATACATGTTTACACCGATATTTGATTTCTGTCGCTATATCTACTGTTTTCGAAAGCG 628

QY 1141 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1200
DB 627 GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTCTTTT 568

QY 1201 GTTGTGTTGGTGAAGATTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 1260
DB 567 GTTGTGTTGGTGAAGATTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACC 508

QY 1261 GGAGTGTAGGAGAGGCTGGTTATGATGCGGAGGAGTGTAGTTTACATAGGGGTC 1320
DB 507 GGAGTGTAGGAGAGGCTGGTTATGATGCGGAGGAGTGTAGTTTACATAGGGGTC 448

QY 1321 ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAG 1380
DB 447 ATAGGTGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAG 388

QY 1381 CATCTCCCTGTCCCTGTGGTGTATCGGGAGCAGGCGCCAGATTAACCTTAACCTTTCT 1440
DB 387 CATCTCCCTGTCCCTGTGGTGTATCGGGAGCAGGCGCCAGATTAACCTTAACCTTTCT 328

QY 1441 TATTCTGTAGTATTAAGAGGCAAGAGCGGGGTTTACCCCTCTCTGGGGGAAGAAA 1500
DB 327 TATTCTGTAGTATTAAGAGGCAAGAGCGGGGTTTACCCCTCTCTGGGGGAAGAAA 268

QY 1501 GTCAATTAATTAATCTCATCATGTCCACCCCGAGGAGGGCTTCTGACTGTGGTTCG 1560
DB 267 GTCAATTAATTAATCTCATCATGTCCACCCCGAGGAGGGCTTCTGACTGTGGTTCG 208

QY 1561 CTTGACAGTATATCCGAAGTCCGGAGAGGGGGTGTGGAAGATGCCATTTTCTCTCT 1620
DB 207 CTTGACAGTATATCCGAAGTCCGGAGAGGGGGTGTGGAAGATGCCATTTTCTCTCT 148

QY 1621 CCAGCGGTAAAGTGGCGGGGTGAGCAGCCAGCGGGCGCGCGAGGATCTGGGCAAG 1680
DB 147 CCAGCGGTAAAGTGGCGGGGTGAGCAGCCAGCGGGCGCGCGAGGATCTGGGCAAG 88
```

QY 1681 ATGCTGCGGGGGGGTGTCTTCTTCTCGTAAAGCCTCTTGGATACGTCATATCTGA 1740  
DB 87 ATGCTGCGGGGGGGTGTCTTCTTCTTCTCGGTAAAGCCTCTTGGATACGTCATATCTGA 28  
QY 1741 AAACGAAGAAGTGGCTGTGAAGTATT 1767  
DB 27 AAACGAAGAAGTGGCTGTGAAGTATT 1  
RESULT 3  
US-09-583-350-8  
; Sequence 8, Application US/09583350  
; Patent No. 6517843  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, et al.  
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS  
; TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2  
; FILE REFERENCE: 454313-2340.1  
; CURRENT APPLICATION NUMBER: US/09/583,350  
; CURRENT FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/151,564  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 1768  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-583-350-8  
Query Match 92.9%; Score 1642.4; DB 4; Length 1768;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 1696; Conservative 0; Mismatches 71; Indels 1; Gaps 1;  
QY 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
DB 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGATATATC 120  
DB 61 AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTCTCACTCTGATATATC 120  
QY 121 CTTCCGAGCAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATATTTTA 180  
DB 121 CTTCCGAGCAGCGGCAAGAAATACGGGATCTTCCAAATATCCCTATTTGATATTTTA 180  
QY 181 TTGTTGGCAGGAGGGAATAGAGAGGACGAAACACCTCACCTCAGGGGTTGCTAATT 240  
DB 181 TTGTTGGCAGGAGGGAATAGAGAGGAGCAACACCTCACCTCAGGGGTTGCTAATT 240  
QY 241 TTGTGAAGAGCAGACTTTTAAAGTGAAGTGTATTTGGTGGCGGCTGCCACATCG 300  
DB 241 TTGTGAAGAGCAGAACTTTTAAAGTGAAGTGTATTTGGTGGCGGCTGCCACATCG 300  
QY 301 AGAAGCGAAGGACAGATCAGCAGAAATAAGATATCTGCAGTAAAGAGCAACTTAC 360  
DB 301 AGAAGCGAAGGACAGATCAGCAGAAATAAGATATTTGCAGTAAAGAGCAACTTAC 360  
QY 361 TGATGAGTGTGAGCTCTAGATCTCAGGGAACAGGAGTGCCTCTACTGCTGA 420  
DB 361 TTATTGAATGTGAGCTCTCTGATCTCAAGGACAGCGGAGTGCCTCTACTGCTGA 420  
QY 421 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTTCAGAGCAGCACCTGTAAAGCTTTG 480  
DB 421 GTACCTTGTGAGAGCGGGAGTCTGTGACCGTTCAGAGCAGCACCTGTAAAGCTTTG 480  
QY 481 TCAGAAATTTCCGCGGCTGGCTGAATTTTGAAGTGAAGCGGGAATAATCGAAGCGGTG 540  
DB 481 TCAGAAATTTCCGCGGCTGGCTGAATTTTGAAGTGAAGCGGGAATAATCGAAGCGGTG 540  
QY 541 ATTGGAAGACTAATGTACAGTCTATTTGGGGGCACTTGGTGGTGAAGCAATGGG 600  
DB 541 ATTGGAAGCAATGTACAGTCTATTTGGGGGCACTTGGTGGTGAAGCAATGGG 600

QY 601 CTGCTAAATTTTGCAGACCCGGAAACCAATATCTGGAACACCACTAGAAACAAGTGGTGGG 660  
DB 601 CTGCTAAATTTTGCAGACCCGGAAACCAATATCTGGAACACCACTAGAAACAAGTGGTGGG 660  
QY 661 ATGGTTACCATGGTGAAGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCTGGTGG 720  
DB 661 ATGGTTACCATGGTGAAGAAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCTGGTGG 720  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATCTGACCTGTAGAGACTAAAGTGGAACTG 780  
DB 721 ATGATCTACTGAGACTGTGTGATCGATATCCATCTGACCTGTAGAGACTAAAGTGGAACTG 780  
QY 781 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTGGTGAATGGTACT 840  
DB 781 TACCTTTTGGCCCGCAGTATTCTGATTACAGCAATCAGACCCCGTGGTGAATGGTACT 840  
QY 841 CTTCAACTCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 900  
DB 841 CTTCAACTCTGTCCAGCTGTAGAAGCTCTCTATCGGAGGATTAATCTCTTGGTATTTT 900  
QY 901 GGAAGATGCTACAGAAACCAATCCAGGAGAAAGGGGCGCAGTTCGTCACCTTTCCCC 960  
DB 901 GGAAGATGCTACAGAAACCAATCCAGGAGAAAGGGGCGCAGTTCGTCACCTTTCCCC 960  
QY 961 CATGCCCTGAAATTTCCATATGAAATAAATTAAGTCTTTTATCACTTCGTAAATGGT 1020  
DB 961 CATGCCCTGAAATTTCCATATGAAATAAATTAAGTCTTTTATCACTTCGTAAATGGT 1020  
QY 1021 TTTTATATTTCA-TTAAAGGTTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGA 1079  
DB 1021 TTTTATATTTCA-TTAAAGGTTTAAAGTGGGGGCTTTTAAAGTCTTTTAAATTTCTCTGAATTTGA 1080  
QY 1080 CATACATGTTTACACGGATATTTGATTTCTGCTGCTGATATCTGTTTTCGAAACGAGTGC 1139  
DB 1081 CATACATGTTTACACGGATATTTGATTTCTGCTGCTGATATTTACTGTTTTCGAAACGAGTGC 1140  
QY 1140 CGAGGCTACGCTGGTCCACATTTCTAGAGGTTTGTAGCCTTCAGCCAAAGCTGATTCCTTT 1199  
DB 1141 CGAGGCTACGCTGGTCCACATTTCTAGAGGTTTGTAGCCTTCAGCCAAAGCTGATTCCTTT 1200  
QY 1200 TGTGTTGTTGCTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTTAAAGTACC 1259  
DB 1201 TGTGTTGTTGCTCGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGTGTAGGTAAC 1260  
QY 1260 GGGAGTGTAGGAGAGGGCTGGGTTATGATGTTGGGGGAGGAGTGTATTTACATATGGGT 1319  
DB 1261 GGGAGTGTAGGAGAGGGCTGGGTTATGATGTTGGGGGAGGAGTGTATTTACATATGGGT 1320  
QY 1320 CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTATCATCTNAAATAACAGACTGGAGC 1379  
DB 1321 CATAGGTGAGGCTGTGGCTTTGTTACAAAGTTATCATCTNAAATAACAGACTGGAGC 1380  
QY 1380 CCATCCCTCTGACCTGGGTGATCGGGAGCAGGCGCCAGAAATTTCAACCTTAACTTTTC 1439  
DB 1381 CCATCCCTCTGACCTGGGTGATCGGGAGCAGGCGCCAGAAATTTCAACCTTAACTTTTC 1440  
QY 1440 TTATTTCTGTAGTATTTCAAGCGGCAACAGCGGGGGTTTGAACCTTCTCTGGGGGAGAA 1499  
DB 1441 TTATTTCTGTAGTATTTCAAGCGGCAACAGCGGGGGTTTGAACCTTCTCTGGGGGAGAA 1500  
QY 1500 AGTCATTAATTTCAATCTCATCTGTCACCGCCAGGAGGGGCTTCTGACTGTGGTTC 1559  
DB 1501 AGTCATTAATTTCAATCTCATCTGTCACCGCCAGGAGGGGCTTCTGACTGTGGTTC 1560  
QY 1560 GCTTGACAGTATATCCGAAAGTGTGGGAGAGCGGGGTGTTGAAGATGCCATTTTTCCTTC 1619  
DB 1561 GCTTGACAGTATATCCGAAAGTGTGGGAGAGCGGGGTGTTGAAGATGCCATTTTTCCTTC 1620  
QY 1620 TCCAGCGGTAAACGTTGGCGGGGGTGGACGACCGAGGGGCGCGGAGGATCTGGGCAA 1679  
DB 1621 TCCAGCGGTAAACGTTGGCGGGGGTGGACGACCGAGGGGCGCGGAGGATCTGGGCAA 1680



QY	1620	TCCAGCGGTAA	CGGTGGCGGGTGGAGCGCCAGCGGGCGCGCGGAGGATCTGGCCAA	1679
DB	1621	TCCAGCGGTAG	CGGTGGCGGGTGGAGCGCCAGCGGGCGCGCGGAGGATCTGGCCAA	1680
QY	1680	GATGGCTGCGGGGCGGTGCTCTTCTTCCTTCGGTAA	CGCTCTTCGGATACGTCATATCTG	1739
DB	1681	GATGGCTGCGGGGCGGTGCTCTTCTTCGGTAA	CGCTCTTCGGATATGTCATAGCTG	1740
QY	1740	AAACGAAAGAGTGGCGTGAAGTATT	1767	
DB	1741	AAACGAAAGAGTGGCGTGAAGTATT	1768	
RESULT 5				
US-10-112-540-1				
; Sequence 1, Application US/10112540				
; Patent No. 6794163				
; GENERAL INFORMATION:				
; APPLICANT: Liu, Qiang				
; APPLICANT: Tikoo, Suresh K.				
; APPLICANT: Willson, Philip				
; APPLICANT: Babik, Lorne A.				
; TITLE OF INVENTION: METHODS TO CULTURE CIRCOVIRUS				
; FILE OF INVENTION: 293102003100				
; CURRENT APPLICATION NUMBER: US/10/112,540				
; CURRENT FILING DATE: 2002-03-27				
; PRIOR APPLICATION NUMBER: US 60/279,173				
; PRIOR FILING DATE: 2001-03-27				
; NUMBER OF SEQ ID NOS: 3				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 1				
; LENGTH: 1768				
; TYPE: DNA				
; ORGANISM: Porcine circovirus				
US-10-112-540-1				
Query Match 91.7%; Score 1620; DB 4; Length 1768;				
Best Local Similarity 95.1%; Pred. No. 0;				
Matches 1682; Conservative 0; Mismatches 85; Indels 1; Gaps 1;				
QY	1	ACCAGCGCACTTCGGCAGCGCGCAGCACCCTCGGCAGCACCTCAGCAGCAACATGCCACGA	60	
DB	1	ACCAGCGCACTTCGGCAGCGCGCAGCACCCTCGGCAGCACCTCAGCAGCAACATGCCACGA	60	
QY	61	AGAAAGTGAAGAGCGGACCCCAACCCCAATAAAGGTGGTTCCTCTGTAATATC	120	
DB	61	AGAAAGTGAAGAGCGGACCCCAACCCCAATAAAGGTGGTTCCTCTGTAATATC	120	
QY	121	CTTCCGAGAGCAGCGCAAGAAATACGGGATCTTCCAAATATCCCTATTGATATTTTA	180	
DB	121	CTTCCGAGAGCAGCGCAAGAAATACGGGATCTTCCAAATATCCCTATTGATATTTTA	180	
QY	181	TTGTTGGCAGGAGGGTAAATGAGAGGACGAACCTCACCTCCAGGGGTTCGCTAAT	240	
DB	181	TTGTTGGCAGGAGGGTAAATGAGAGGACGAACCTCACCTCCAGGGGTTCGCTAAT	240	
QY	241	TTGTGAGAGCAGCACTTTTAAATAAGTGAAGTATTGGGTGCCCGCTCCACATCG	300	
DB	241	TTGTGAGAGCAGCACTTTTAAATAAGTGAAGTATTGGGTGCCCGCTCCACATCG	300	
QY	301	AGAAAGCGAAAGGACAGATCAGCAGAAATAAGAAATATGTCAGTAAAGAGCAACTTAC	360	
DB	301	AGAAAGCGAAAGGACAGATCAGCAGAAATAAGAAATATGTCAGTAAAGAGCAACTTAC	360	
QY	361	TGATGAGTGTGGAGCTCTAGATCTCAGGACAAACGGAGTACCTGTCTACTGTGTGA	420	
DB	361	TTATTGAAATGTGGAGCTCTCTGATCTCAAGACAAACGGAGTACCTGTCTACTGTGTGA	420	
QY	421	GTACCTCTGTGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG	480	
DB	421	GTACCTCTGTGAGAGCGGGATCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG	480	

1561 CCTTGACAGTATATCCGAAGGTGCGGAGAGCGGGTGTGAAGATGCCATTTTCCTTC 1620  
1620 TCCAGCGGTACGGTGGCGGGTGGAGCGCCAGGGCGGGCGGAGGATCGGCCAA 1679  
1621 TCCAAAGGTAGCGGTGGCGGGGTGGAGCGAGCCAGGGCGGGCGGAGGATCGGCCAA 1680  
1680 GATGCTCGGGGGCGGTGTCTTCTTCTTGGTAACGCTCTCCGTGATACGCTCATATCTG 1739  
1681 GATGCTCGGGGGCGGTGTCTTCTTCTTGGTAACGCTCTCCGTGATACGCTCATATCTG 1740  
1740 AAAACGAAAGAGTGGCTGTAAATTT 1767  
1741 AAAACGAAAGAGTGGCTGTAAATTT 1768

RESULT 6  
US-09-347-594-1  
; Sequence 1, Application US/09347594  
; Patent No. 6217883  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon M.  
; APPLICANT: MEEHAN, Brian M.  
; APPLICANT: ELLIS, John A.  
; APPLICANT: KRAKOWKA, George S.  
; APPLICANT: AUDONNET, Jean-Christophe F.  
; TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARVOVIRUS VACCINE  
; FILE REFERENCE: 454313-2338  
; CURRENT APPLICATION NUMBER: US/09/347,594  
; CURRENT FILING DATE: 1999-07-01  
; EARLIER APPLICATION NUMBER: 98 08777  
; EARLIER FILING DATE: 1998-07-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-347-594-1

Query Match 79.9%; Score 1412; DB 3; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ACCAGCGCACTTCGGCAGCGGAGCACCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
348 ACCAGCGCACTTCGGCAGCGGAGCACCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 407  
61 AGAAGAAATGGAAGAGCGGACCCCAACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 120  
408 AGAAGAAATGGAAGAGCGGAGCACCACCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC 467  
121 CTTCCGAAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTATTTA 180  
468 CTTCCGAAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTATTTA 527  
181 TTGTTGGCAGGAGGATTAAGAGGAGGAGCAGCACCCTCAGGAGGTTGCGCTAATTT 240  
528 TTGTTGGCAGGAGGATTAAGAGGAGGAGCAGCACCCTCAGGAGGTTGCGCTAATTT 587  
241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTGTTGGTGGCCGCTGCCACATCG 300  
588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGTATTGTTGGTGGCCGCTGCCACATCG 647  
301 AGAAGCGAAGGAGGAGCAGATCAGCAGAAATAAGAAATATCGCAGTAAGAGGCAACTTAC 360  
648 AGAAGCGAAGGAGGAGCAGATCAGCAGAAATAAGAAATATCGCAGTAAGAGGCAACTTAC 707  
361 TGATGGAGTGTGAGGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 420  
708 TGATGGAGTGTGAGGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 767  
421 GTACCTTGTGGAGAGCGGAGTCTGGTGACCGTTGCGAGAGCAGCACCCTGTAAACGTTTG 480

768 GTACCTTGTGGAGAGCGGGAGTCTGGTGACCGTTGCGAGAGCAGACCCTCTGAACGTTTG 827  
481 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATAATGAGAGCGTG 540  
828 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAAGCGGGAATAATGAGAGCGTG 887  
541 ATTGGAAGACTAATGTACAGCTCAATGTGGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 600  
888 ATTGGAAGACTAATGTACAGCTCAATGTGGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 947  
601 CTGCTAATTTTGCAGACCCGGAACCACTACTCGMAACCACTAGAAACAAAGTGGTGGG 660  
948 CTGCTAATTTTGCAGACCCGGAACCACTACTCGMAACCACTAGAAACAAAGTGGTGGG 1007  
661 ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720  
1008 ATGGTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
721 ATGATCTACTGAGACTGTGTGATCGATATCATTTGATGACTGTGAGAGCTAAAGTGGAACTG 780  
1068 ATGATCTACTGAGACTGTGTGATCGATATCATTTGATGACTGTGAGAGCTAAAGTGGAACTG 1127  
781 TACCTTTTGGCGCGCAGTATCTGATTACCAATCAGACCCCTGGTGAATGCTACT 840  
1128 TACCTTTTGGCGCGCAGTATCTGATTACCAATCAGACCCCTGGTGAATGCTACT 1187  
841 CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTTATCGGAGGATTACTTCTTGGTATTTT 900  
1188 CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTTATCGGAGGATTACTTCTTGGTATTTT 1247  
901 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCCTACCCCTTCCCGCC 960  
1248 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGCGAGTTCCTACCCCTTCCCGCC 1307  
961 CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTATCACTTCTGTAATGCT 1020  
1308 CATGCCCTGAATTTCCATATGAATAAATTAATGAGTCTTTTATCACTTCTGTAATGCT 1367  
1021 TTTTATTTATTAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGTAC 1080  
1368 TTTTATTTATTAAGGTTAAAGTGGGGGCTTTTAAATTTAAATTTCTCTGAATTTGTAC 1427  
1081 AFACATGTTTACAGGATATTTGATTTCTGTCGATATATCTGTTTTCGAAACGAGTGCC 1140  
1428 AFACATGTTTACAGGATATTTGATTTCTGTCGATATATCTGTTTTCGAAACGAGTGCC 1487  
1141 GAGGCTTACGTCGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT 1200  
1488 GAGGCTTACGTCGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT 1547  
1201 GTTGTGTTGTTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260  
1548 GTTGTGTTGTTGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607  
1261 GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGGAGGAGTATTTATATAGGGGTC 1320  
1608 GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGGAGGAGTATTTATATAGGGGTC 1667  
1321 ATAGTGGAGGGCTGTGGCCCTTTTGTACAAAGTTTATCATCTAAATAACAGCACTGGAGCC 1380  
1668 ATAGTGGAGGGCTGTGGCCCTTTTGTACAAAGTTTATCATCTAGAATAACAGCACTGGAGCC 1727  
1381 CACTCCCTGTCCACCTGGGTGATCGGGAGCAGGGGCCAG 1420  
1728 CACTCCCTGTCCACCTGGGTGATCGGGAGCAGGGGCCAG 1767

## RESULT 7

US-09-082-558-1  
; Sequence 1, Application US/09082558A  
; Patent No. 6368601  
; GENERAL INFORMATION:





;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/082,558  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 9800873  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 9803707  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PR 97/12382  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03  
;; NUMBER OF SEQ ID NOS: 6  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 1  
;; LENGTH: 1767  
;; TYPE: DNA  
;; ORGANISM: Porcine circovirus  
US-09-161-092-1

Query Match 79.9%; Score 1412; DB 3; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGGCACTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 60  
DB 348 ACCAGGCACTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 407

QY 61 AGAAGAATGGAAGAAGCGGACCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 120  
DB 408 AGAAGATGGAAGAAGCGGACCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 467

QY 121 CTTCCGAAGCAGGCGCAAGAAAATACGGGATCTTCCAAATATCCCTATTTGATTTTAA 180  
DB 468 CTTCCGAAGCAGGCGCAAGAAAATACGGGATCTTCCAAATATCCCTATTTGATTTTAA 527

QY 181 TTGTGGCAGGAGGTATAGGAGGACGACCACTCACCTCCAGGGGTTTCGCTAAT 240  
DB 528 TTGTGGCAGGAGGTATAGGAGGACGACCACTCACCTCCAGGGGTTTCGCTAAT 587

QY 241 TTGTGAAGAAGCAGACTTTTAAAGTGAAGTGGTATTTGGGTGCCCCGCTCCACATCG 300  
DB 588 TTGTGAAGAAGCAGACTTTTAAAGTGAAGTGGTATTTGGGTGCCCCGCTCCACATCG 647

QY 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 360  
DB 648 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAAGAGGCAACTTAC 707

QY 361 TGATGAGTGTGAGTCTCTAGATCTCAGGACCAAGGATGACCTGTCTACTGTCTGCA 420  
DB 708 TGATGAGTGTGAGTCTCTAGATCTCAGGACCAAGGATGACCTGTCTACTGTCTGCA 767

QY 421 GTACCTTTTGGAGCGGGAGTCTGTCACCGTTCAGAGCAGCACCCCTGTAACGTTTG 480  
DB 768 GTACCTTTTGGAGCGGGAGTCTGTCACCGTTCAGAGCAGCACCCCTGTAACGTTTG 827

QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAAAATGCAAGACGCTG 540  
DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTTGAAGTGAAGCGGAAAAATGCAAGACGCTG 887

QY 541 ATTGGAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGTGTAAGCAATGGG 600  
DB 888 ATTGGAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGTGTAAGCAATGGG 947

QY 601 CTGCTAATTTTGCAGACCGGAAACCACTACTGGAACCCACCTAGAAACAAAGTGGTGG 660  
DB 948 CTGCTAATTTTGCAGACCGGAAACCACTACTGGAACCCACCTAGAAACAAAGTGGTGG 1007

QY 661 ATGGTTTACCATGTTGAAGAGTGGTTTATTTGATGACTTTTATGGCTGCCCTGGG 720  
DB 1008 ATGGTTTACCATGTTGAAGAGTGGTTTATTTGATGACTTTTATGGCTGCCCTGGG 1067

QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTTAAAGTGGAACTG 780  
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGACTGTAGAGACTTAAAGTGGAACTG 1127

QY 781 TACCTTTTTTGGCCCGCAGTATTCTGATTTACCAGCAATCAGACCCCGTTTGGATGGTACT 840

DB 1128 TACCTTTTTTGGCCCGCAGTATTCTGATTAACCAATCAGACCCCGTTGGAATGGTACT 1187  
QY 841 CCTCAACTGCTGTCGCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900  
DB 1188 CCTCAACTGCTGTCGCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 1247  
QY 901 GGAAGAATGTCTACAGAACAAATCCACGGAGGAAGGGGCGCAGTTCGTACCCCTTTCCCGCC 960  
DB 1248 GGAAGAATGTCTACAGAACAAATCCACGGAGGAAGGGGCGCAGTTCGTACCCCTTTCCCGCC 1307  
QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020  
DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367  
QY 1021 TTTTATTATTCAATTAAGGTTAAAGTGGGGGCTCTTTAAAAATTAATTAATTAATTAATTAATTAAT 1080  
DB 1368 TTTTATTATTCAATTAAGGTTAAAGTGGGGGCTCTTTAAAAATTAATTAATTAATTAATTAATTAAT 1427  
QY 1081 ATACATGTTTACACGGATATTTGATTTCTGTGCTGATATATCTGTTTTCGAACGCGAGTCC 1140  
DB 1428 ATACATGTTTACACGGATATTTGATTTCTGTGCTGATATATCTGTTTTCGAACGCGAGTCC 1487  
QY 1141 GAGGCTACGTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1200  
DB 1488 GAGGCTACGTGCTTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTTT 1547  
QY 1201 GTTGTTCGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1260  
DB 1548 GTTGTTCGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1607  
QY 1261 GGAGTGTAGGAGAGGCTGGGTTATGTTATGCGGAGGAGTATGTTTACATAGGGTTC 1320  
DB 1608 GGAGTGTAGGAGAGGCTGGGTTATGTTATGCGGAGGAGTATGTTTACATAGGGTTC 1667  
QY 1321 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTATCATCTAAATAACAGCACTGGAGCC 1380  
DB 1668 ATAGTGTAGGCTGTGGCTTTGTTACAAAGTATCATCTAAATAACAGCACTGGAGCC 1727

QY 1381 CACTCCCTGTCCACCTGGGTGATCGGGGAGCAGGCGCCAG 1420  
DB 1728 CACTCCCTGTCCACCTGGGTGATCGGGGAGCAGGCGCCAG 1767

RESULT 9

US-09-583-350-1  
; Sequence 1, Application US/09583350  
; Patent No. 6517843  
; GENERAL INFORMATION:  
; APPLICANT: Ellis, et al.  
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION A  
; TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2  
; FILE REFERENCE: 454313-2340.1  
; CURRENT APPLICATION NUMBER: US/09/583,350  
; CURRENT FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: 60/151,564  
; PRIOR FILING DATE: 1999-08-31  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-583-350-1

Query Match 79.9%; Score 1412; DB 4; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACCAGGCACTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 60  
DB 348 ACCAGGCACTTCGGCAGCGGCGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 407

```
QY 61 AGAAGATGGAAGACGACGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGACGACGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 467
QY 121 CTTCCGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 180
DB 468 CTTCCGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 527
QY 181 TTGTTGGCGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 528 TTGTTGGCGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 587
QY 241 TTGTTGAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
DB 588 TTGTTGAAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 647
QY 301 AGAAGCGAAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 360
DB 648 AGAAGCGAAAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 707
QY 361 TGATGGAGTGGAGCTCTAGATCTCAGGACGACGACGACGACGACGACGACGACGACGACG 420
DB 708 TGATGGAGTGGAGCTCTAGATCTCAGGACGACGACGACGACGACGACGACGACGACGACG 767
QY 421 GTACCTTGTGGAGCGGAGTCTGGTGACCGTTGCAGACGACGACGACGACGACGACGACGACG 480
DB 768 GTACCTTGTGGAGCGGAGTCTGGTGACCGTTGCAGACGACGACGACGACGACGACGACGACG 827
QY 481 TCAGAAATTTCCGGGGTGGCTGAATCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 540
DB 828 TCAGAAATTTCCGGGGTGGCTGAATCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 887
QY 541 ATTGGAACACTAATGTACACGTCATCTGGGGCCACCTGGGTGGTGAAGCAAAATGGG 600
DB 888 ATTGGAACACTAATGTACACGTCATCTGGGGCCACCTGGGTGGTGAAGCAAAATGGG 947
QY 601 CTGCTAAATTTGCAGACCGGAAACCACTACTGGAACCACTAGAAACCAAGTGGTGGG 660
DB 948 CTGCTAAATTTGCAGACCGGAAACCACTACTGGAACCACTAGAAACCAAGTGGTGGG 1007
QY 661 ATGGTTACCTGTTGGAAGTGGTGGTGAATGATGACTTTTATGATGACTTTTATGATGACTTT 720
DB 1008 ATGGTTACCTGTTGGAAGTGGTGGTGAATGATGACTTTTATGATGACTTTTATGATGACTTT 1067
QY 721 ATGATCTACTGAGACTGTGATCCATATCCATTCGACTGAGAGCTAAAGTGAAGTGA 780
DB 1068 ATGATCTACTGAGACTGTGATCCATATCCATTCGACTGAGAGCTAAAGTGAAGTGA 1127
QY 781 TACCTTTTGTGGCCGCGAGTATCTGATTAACGCAATCAGACCCCGTTGGAATGGTACT 840
DB 1128 TACCTTTTGTGGCCGCGAGTATCTGATTAACGCAATCAGACCCCGTTGGAATGGTACT 1187
QY 841 CTTCAACTGCTGTCCTCCAGCTGAGAGCTTTTATCGGAGGATTAATCTTCCCTGGTGAATTT 900
DB 1188 CTTCAACTGCTGTCCTCCAGCTGAGAGCTTTTATCGGAGGATTAATCTTCCCTGGTGAATTT 1247
QY 901 GGAAGATGCTACAGAAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 1248 GGAAGATGCTACAGAAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1307
QY 961 CATGCCCTGAAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 1308 CATGCCCTGAAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTAATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTAATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAATTAAT 1427
QY 1081 ATACATGGTTACCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140
DB 1428 ATACATGGTTACCGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1487
QY 1141 GAGGCTTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTCTTTCTTTT 1200
```

```
DB 1488 GAGGCTTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTCTTTT 1547
QY 1201 GTTGTGTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1260
DB 1548 GTTGTGTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1607
QY 1261 GGAAGTGTAGGAGGAGGCTGGGTATGTTATGCGGAGGAGTGTATCATATAGGAGGTC 1320
DB 1608 GGAAGTGTAGGAGGAGGCTGGGTATGTTATGCGGAGGAGTGTATCATATAGGAGGTC 1667
QY 1321 ATAGGTGAGGAGGCTGGGTCTTTTCAAAAGTTATCATCTAAATTAACAGCCTTGAGGCC 1380
DB 1668 ATAGGTGAGGAGGCTGGGTCTTTTCAAAAGTTATCATCTAAATTAACAGCCTTGAGGCC 1727
QY 1381 CACTCCCTCTGACCCCTGGGTGATCGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTCTGACCCCTGGGTGATCGGGAGCAGGGCCAG 1767
```

## RESULT 10

```
US-09-884-514-1
; Sequence 1, Application US/09884514
; Patent No. 6660272
; GENERAL INFORMATION:
; APPLICANT: MEEHAN, Brian
; APPLICANT: ALLAN, Gordon
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
; APPLICANT: NEWTONARDS, Francis McNeilly
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/884,514
; CURRENT FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: FR 9800873
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: FR 9803707
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: FR 97/12382
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-884-514-1
```

```
Query Match 79.9%; Score 1412; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 ACCAGCGCACTTCGGCAGCGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGCGCACTTCGGCAGCGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGGTGTTCACTCTGAATAATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCCAATAAAAGTGGGTGTTCACTCTGAATAATC 467
QY 121 CTTCCGAGACGACGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTTTAA 180
DB 468 CTTCCGAGACGACGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTTTAA 527
QY 181 TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCAGCTCCAGGGGTTCCCTAATT 240
DB 528 TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACACCTCAGCTCCAGGGGTTCCCTAATT 587
```



```
Db 888 ATTGAAGACTAATGTACAGCTCATTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 947
Qy 601 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Db 948 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 1007
Qy 661 ATGTTACCATGTTGAAGAGTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGG 720
Db 1008 ATGTTACCATGTTGAAGAGTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGG 1067
Qy 721 ATGTTACCATGTTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGGTGGTGG 780
Db 1068 ATGTTACCATGTTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGGTGGTGG 1127
Qy 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 840
Db 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCGTTGGAATGGTACT 1187
Qy 841 CCTCAACTGCTGTCACAGCTGTAGAGCTCTTTATCGAGGATTAATCTTCTGTTATTTT 900
Db 1188 CCTCAACTGCTGTCACAGCTGTAGAGCTCTTTATCGAGGATTAATCTTCTGTTATTTT 1247
Qy 901 GGAAGATGCTACAGAAACAATCCACGAGGAGGGGGCCAGTTGTCACCCCTTTCCCGCCC 960
Db 1248 GGAAGATGCTACAGAAACAATCCACGAGGAGGGGGCCAGTTGTCACCCCTTTCCCGCCC 1307
Qy 961 CATGCCCTGAATTTCCATATGAAATTAATTAATGAGTCTTTTATGCTGCTGTAATGGT 1020
Db 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATGAGTCTTTTATGCTGCTGTAATGGT 1367
Qy 1021 TTTTATTTATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAAT 1080
Db 1368 TTTTATTTATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTAAT 1427
Qy 1081 ATACATGTTTACACGGATTTGATTTCTGTTGCTGATATATCTGTTTTCGAAACGAGTGCC 1140
Db 1428 ATACATGTTTACACGGATTTGATTTCTGTTGCTGATATATCTGTTTTCGAAACGAGTGCC 1487
Qy 1141 GAGGCTACGTTGCTGATATATTTCCAGAGTTTGTAGTCTGACCCACAGCTGTTTCTTTT 1200
Db 1488 GAGGCTACGTTGCTGATATATTTCCAGAGTTTGTAGTCTGACCCACAGCTGATTTCTTTT 1547
Qy 1201 GTTGTGTTGGTGGAGTAAATCAATAGTAAATCTAGGACAGTTTGGGGGTAAAGTACCG 1260
Db 1548 GTTGTGTTGGTGGAGTAAATCAATAGTAAATCTAGGACAGTTTGGGGGTAAAGTACCG 1607
Qy 1261 GGAGTGTAGGAGAGGGCTGGGTTATGTTATGGCGGAGGAGTAGTTTACATAGGGGTC 1320
Db 1608 GGAGTGTAGGAGAGGGCTGGGTTATGTTATGGCGGAGGAGTAGTTTACATAGGGGTC 1667
Qy 1321 ATAGGTAGGGCTGTGGCTTTTGTACAAAGTTTATCACTAAATTAACAGCACTGGAGCC 1380
Db 1668 ATAGGTAGGGCTGTGGCTTTTGTACAAAGTTTATCACTAAATTAACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTCACTCCCTGATCGGGGAGCAGGSCCAG 1420
Db 1728 CACTCCCTGTCACTCCCTGATCGGGGAGCAGGSCCAG 1767
```

## RESULT 12

```
US-09-082-558-2
; Sequence 2, Application US/09082558A
; Patent No. 638601
; GENERAL INFORMATION:
; APPLICANT: ALLAN, Gordon
; APPLICANT: MEEHAN, Brian
; APPLICANT: CLARK, Edward
; APPLICANT: HAINES, Deborah
; APPLICANT: HASSARD, Lori
; APPLICANT: HARDING, John
; APPLICANT: CHARREYRE, Catherine E.
; APPLICANT: CHAPPUIS, Gilles E.
```

```
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
; FILE REFERENCE: ALLAN
; CURRENT APPLICATION NUMBER: US/09/082,558A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: FR 9800873
; EARLIER FILING DATE: 1998-01-22
; EARLIER APPLICATION NUMBER: FR 9803707
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: FR 97/12382
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
; US-09-082-558-2
```

```
Query Match 79.8%; Score 1410.4; DB 3; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 60
Db 348 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGGAGCAGCACCTCAGCAGCAACATGCCAGCA 407
Qy 61 AGAAGATGAAGAGGAGGAGCCCAACCCCATAAAGTGGTGGTTCACCTCTGAATAATC 120
Db 408 AGAAGATGAAGAGGAGGAGCCCAACCCCATAAAGTGGTGGTTCACCTCTGAATAATC 467
Qy 121 CTTCCGAAGACGAGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTATTTTA 180
Db 468 CTTCCGAAGACGAGCGCAAGAAATACGGATCTTCCAATATCCCTATTTGATTATTTTA 527
Qy 181 TTGTTGGCAGGAGGGTAAATGAGAGGAGCAACACCTCACCTCCAGGGGTTGCTTAATT 240
Db 528 TTGTTGGCAGGAGGGTAAATGAGAGGAGCAACACCTCACCTCCAGGGGTTGCTTAATT 587
Qy 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300
Db 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647
Qy 301 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTCCAGTAAAGAGGCAACTTAC 360
Db 648 AGAAAGCGAAAGGAAACAGATCAGCAGAAATAAGAAATCTCCAGTAAAGAGGCAACTTAC 707
Qy 361 TGATGGAGTGTGGAGTCTTAGATCTCAGGCAACCGAGTACCTGTCTACTGCTGTA 420
Db 708 TGATGGAGTGTGGAGTCTTAGATCTCAGGCAACCGAGTACCTGTCTACTGCTGTA 767
Qy 421 GTACCTTTGGAGAGCGGGAGTCTGGTGACCGTTGAGAGCAGCAGCCTGTAACTGTTG 480
Db 768 GTACCTTTGGAGAGCGGGAGTCTGGTGACCGTTGAGAGCAGCAGCCTGTAACTGTTG 827
Qy 481 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGAGTGAAGGAGGAGGAGGAGGAGG 540
Db 828 TCAGAAATTTCCGCGGGCTGGCTGAACCTTTTGAAGAGTGAAGGAGGAGGAGGAGGAGG 887
Qy 541 ATTGGAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGGTGGTAAAGCAAAATGGG 600
Db 888 ATTGGAAGACTAATGTACAGTCAATTTGGGGCCACCTGGGTGGTGGTAAAGCAAAATGGG 947
Qy 601 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 660
Db 948 CTGCTAATTTTGCAGACCCGGAACCAATCTGGAACCACTAGAAACCAAGTGGTGGG 1007
Qy 661 ATGTTACCATGTTGAAGAGTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGG 720
Db 1008 ATGTTACCATGTTGAAGAGTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGG 1067
Qy 721 ATGTTACCATGTTGGTGTATGATGACTTTTATGCTGGTGGTGGTGGTGGTGGTGG 780
```



```
Db 1248 GGAAGAATGCTACAGAAACAATCCACGGAGGAGGGGCGAGTTCCTCCCTTTCCTCC 1307
Qy 961 CATGCCCTGAATTTCCATATGAAATAAATACTAGTCTTTTATACCTTCGTAAATGGT 1020
Db 1308 CATGCCCTGAATTTCCATATGAAATAAATACTAGTCTTTTATACCTTCGTAAATGGT 1367
Qy 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATTTCTCTGAATTTGAC 1080
Db 1368 TTTTATTATTCAATTAAGGTTAAGTGGGGGTCTTTAAAGATTAAATTTCTCTGAATTTGAC 1427
Qy 1081 ATACATGGTTACAGGATATTTGTTCTCTGCTGATATATCTGTTTTCGAACGAGTGGCC 1140
Db 1428 ATACATGGTTACAGGATATTTGTTCTCTGCTGATATATCTGTTTTCGAACGAGTGGCC 1487
Qy 1141 GAGGCTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGTGGTTCTTTT 1200
Db 1488 GAGGCTACGTTGCTACATTTCCAGTATTTTCCAGTAGTTTGTAGTCTCAGCCACAGTGA 1547
Qy 1201 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
Db 1548 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1607
Qy 1261 GGAGTGTAGGAGAGGGCTGGTTATGTTATGTTATGCGGAGGAGTAGTTTACATAGGGTGC 1320
Db 1608 GGAGTGTAGGAGAGGGCTGGTTATGTTATGTTATGCGGAGGAGTAGTTTACATAGGGTGC 1667
Qy 1321 ATAGTGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380
Db 1668 ATAGTGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1727
Qy 1381 CACTCCCTGTCACTCTGGTGTATCGGGAGGAGGAGCCAG 1420
Db 1728 CACTCCCTGTCACTCTGGTGTATCGGGAGGAGGAGCCAG 1767

RESULT 14
US-09-583-350-2
; Sequence 2, Application US/09583350
; Patent No. 6517843
; GENERAL INFORMATION:
; APPLICANT: Ellis, et al.
; TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS
; FILE OF INVENTION: WITH PORCINE CIRCOVIRUS-2
; FILE REFERENCE: 454313-2340.1
; CURRENT FILING DATE: 2000-05-31
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-583-350-2

Query Match 79.8%; Score 1410.4; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGCGCACTTCGGCAGGCGGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 60
Db 348 ACCAGCGCACTTCGGCAGGCGGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCGAGCA 407
Qy 61 AGAAGAATGGAAGAAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 120
Db 408 AGAAGAATGGAAGAAGCGGACCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC 467
Qy 121 CTTCCGAGAGCGGCGGAGAAATACGGGATCTTCCAAATATCCCTATTGATTATTTTA 180
Db 468 CTTCCGAGAGCGGCGGAGAAATACGGGATCTTCCAAATATCCCTATTGATTATTTTA 527
```

```
Qy 181 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAACACCTCACTCCAGGGGTTTCGCTAAT 240
Db 528 TTGTTGGCGAGGAGGTAAATGAGGAAGGACGAACACCTCACCTCCAGGGGTTTCGCTAAT 587
Qy 241 TTGTTGAAGAAGCAGACTTTTAAATGAAGTGAAGTGTATTTGGTCCCGCTGCCACATCG 300
Db 588 TTGTTGAAGAAGCAGACTTTTAAATGAAGTGAAGTGTATTTGGTCCCGCTGCCACATCG 647
Qy 301 AGAAACGCAAGAAAGCAACAGATCAGCAGAAATAAAGAAATCTGCAAGTAAAGAAAGCAACTTAC 360
Db 648 AGAAACGCAAGAAAGCAACAGATCAGCAGAAATAAAGAAATCTGCAAGTAAAGAAAGCAACTTAC 707
Qy 361 TGAATGAGTGTGGAGTCTCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGCTGCA 420
Db 708 TGAATGAGTGTGGAGTCTCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGCTGCA 767
Qy 421 GTACCTTGTGGAGAGCGGAGTCTGTCACCGTTGTCAGAGCAGCACCCTGTAAACGTTTG 480
Db 768 GTACCTTGTGGAGAGCGGAGTCTGTCACCGTTGTCAGAGCAGCACCCTGTAAACGTTTG 827
Qy 481 TCAGAAATTTCCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATAATGCAAGAGCGTG 540
Db 828 TCAGAAATTTCCCGCGGCTGGCTGAACTTTTGAAGTGAAGCGGAAATAATGCAAGAGCGTG 887
Qy 541 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGTGTGTAAGCAAAATGGG 600
Db 888 ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGTGTGTAAGCAAAATGGG 947
Qy 601 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACACACCTAGAAACAAAGTGGTGG 660
Db 948 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACACACCTAGAAACAAAGTGGTGG 1007
Qy 661 ATGTTTACCATTGTTGAAGAGTGGTTTATTTGATCACTTTTATGCTGGCTGGCTCCCTGG 720
Db 1008 ATGTTTACCATTGTTGAAGAGTGGTTTATTTGATCACTTTTATGCTGGCTGGCTCCCTGG 1067
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAGGTGGAACCTG 780
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAGGTGGAACCTG 1127
Qy 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 840
Db 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATCAGACCCCGTTGGAATGGTACT 1187
Qy 841 CCTCAACTGCTGTCCCACTGTAGAAGCTCTTTATCGGAGGATTAATCTCTGGTATTTT 900
Db 1188 CCTCAACTGCTGTCCCACTGTAGAAGCTCTTTATCGGAGGATTAATCTCTGGTATTTT 1247
Qy 901 GGAAGAATGTACAGAAACATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 1248 GGAAGAATGTACAGAAACATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1307
Qy 961 CATGCCCTGAATTTCCATATGAAATAAATACTAGTCTTTTATCACTTCGTAAATGGT 1020
Db 1308 CATGCCCTGAATTTCCATATGAAATAAATACTAGTCTTTTATCACTTCGTAAATGGT 1367
Qy 1021 TTTTATTATTCAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTAATTTCTCTGAATTTGAC 1080
Db 1368 TTTTATTATTCAATTAAGGTTAAGTGGGGGTCTTTAAAGATTAAATTTCTCTGAATTTGAC 1427
Qy 1081 ATACATGGTTACAGGATATTTGTTCTCTGCTGATATATCTGTTTTCGAACGAGTGGCC 1140
Db 1428 ATACATGGTTACAGGATATTTGTTCTCTGCTGATATATCTGTTTTCGAACGAGTGGCC 1487
Qy 1141 GAGGCTACGTTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGTGGTTCTTTT 1200
Db 1488 GAGGCTACGTTGCTACATTTCCAGTATTTTCCAGTAGTTTGTAGTCTCAGCCACAGTGA 1547
Qy 1201 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1260
Db 1548 GTTGTGTTGGTGAAGTAAATCAATAGTGAATCTAGGACAGTTTGGGGTAAAGTAGCG 1607
Qy 1261 GGAGTGTAGGAGAGGGCTGGTTATGTTATGTTATGCGGAGGAGTAGTTTACATAGGGTGC 1320
```

Db 1608 GGAGGTAGGAGAGGGCTGGTATGATGCGGAGGAGTAGTTTACATAGGGTC 1667  
Qy 1321 ATAGGTAGGGCTGGGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC 1380  
Db 1668 ATAGGTAGGGCTGGGCTTTGTTACAAAGTTATCATCTAGAAATACAGCACTGGAGCC 1727  
Qy 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1420  
Db 1728 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1767

RESULT 15  
US-09-884-514-2  
; Sequence 2, Application US/09884514  
; Patent No. 6660272  
; GENERAL INFORMATION:  
; APPLICANT: ALLAN, Gordon  
; APPLICANT: MEEHAN, Brian  
; APPLICANT: CLARK, Edward  
; APPLICANT: HAINES, Deborah  
; APPLICANT: HASSARD, Lori  
; APPLICANT: HARDING, John  
; APPLICANT: CHARREYRE, Catherine E.  
; APPLICANT: CHAPPUIS, Gilles E.  
; APPLICANT: NEWTONARDS, Francis McNeilly  
; TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC  
; TITLE OF INVENTION: REAGENTS  
; FILE REFERENCE: ALLAN  
; CURRENT APPLICATION NUMBER: US/09/884,514  
; CURRENT FILING DATE: 2000-06-19  
; PRIOR APPLICATION NUMBER: FR 9800873  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: FR 9803707  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: FR 97/12382  
; PRIOR FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 1767  
; TYPE: DNA  
; ORGANISM: Porcine circovirus  
US-09-884-514-2

Query Match 79.8%; Score 1410.4; DB 4; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ACCAGGCACTTCGGCAGCGGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 60  
Db 348 ACCAGGCACTTCGGCAGCGGAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGCA 407  
Qy 61 AGAAGAAATGGAAGAGCGGAGCCCAACCCCAATAAAAGTGGGTGTTCACTCTGAATAATC 120  
Db 408 AGAAGAAATGGAAGAGCGGAGCCCAACCCCAATAAAAGTGGGTGTTCACTCTGAATAATC 467  
Qy 121 CTTCCGAGAGCGGAGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 180  
Db 468 CTTCCGAGAGCGGAGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTTA 527  
Qy 181 TTGTTCCGAGGAGGTAATGAGGAGGAGCAACCTCACCTCCAGGGGTTTCGCTAAAT 240  
Db 528 TTGTTCCGAGGAGGTAATGAGGAGGAGCAACCTCACCTCCAGGGGTTTCGCTAAAT 587  
Qy 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGTGCCTGCCACATCG 300  
Db 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGTGCCTGCCACATCG 647  
Qy 301 AGAAGCGAAGAAACAGATACGAGAAATAAGAAATACCTGAGTAAAGAGGCAACTTAC 360  
Db 648 AGAAGCGAAGAAACAGATACGAGAAATAAGAAATACCTGAGTAAAGAGGCAACTTAC 707

Qy 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGCTGTGA 420  
Db 708 TGATGGAGTGTGGAGCTCCTAGATCTCAGGGAACAACGAGTGACCTGTCTACTGCTGTGA 767  
Qy 421 GTACCTTGTTCGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTGAAGCTTTG 480  
Db 768 GTACCTTGTTCGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTGAAGCTTTG 827  
Qy 481 TCAGAAATTTCCGGGGCTGGCTGAACCTTTTGAAGTGAAGCGGGAATAACGAGAGCGTG 540  
Db 828 TCAGAAATTTCCGGGGCTGGCTGAACCTTTTGAAGTGAAGCGGGAATAACGAGAGCGTG 887  
Qy 541 ATTGGAAGACTAAATGTACACGTCAATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 600  
Db 888 ATTGGAAGACTAAATGTACACGTCAATTGTGGGGCCACCTGGGTGTGGTAAAGCAATGGG 947  
Qy 601 CTGCTAAATTTTCAGAGCCCGGAACACATCTCTGAAACACCACTAGAAACAGTGGTGGG 660  
Db 948 CTGCTAAATTTTCAGAGCCCGGAACACATCTCTGAAACACCACTAGAAACAGTGGTGGG 1007  
Qy 661 ATGTTTACCATGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720  
Db 1008 ATGTTTACCATGGTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGTGGNACTG 780  
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCAATGACTGTAGAGACTAAAGTGGNACTG 1127  
Qy 781 TACCTTTTTCGGCCCGCAGTATTCGATTACCAGCAATCAGACCCCTTGGAAATGGTACT 840  
Db 1128 TACCTTTTTCGGCCCGCAGTATTCGATTACCAGCAATCAGACCCCTTGGAAATGGTACT 1187  
Qy 841 CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900  
Db 1188 CCTCAACTGCTGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 1247  
Qy 901 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCGTACCCCTTCCCCCCC 960  
Db 1248 GGAAGAAATGCTACAGAAACAATCCAGGAGGAGGGGGCAGTTCGTACCCCTTCCCCCCC 1307  
Qy 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCACTTCGTAATGCT 1020  
Db 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCACTTCGTAATGCT 1367  
Qy 1021 TTTTATTTATTTAAGGGTTAAGTGGGGGCTCTTTTAAATTAATAATTTCTCTGAATTTGAC 1080  
Db 1368 TTTTATTTATTTAAGGGTTAAGTGGGGGCTCTTTAAGATTAATAATTTCTCTGAATTTGAC 1427  
Qy 1081 ATACATGGTTACACGGATATTGTAATTCCTGGTCTGTATATACCTGTTTCGAAACGAGTGC 1140  
Db 1428 ATACATGGTTACACGGATATTGTAATTCCTGGTCTGTATATACCTGTTTCGAAACGAGTGC 1487  
Qy 1141 GAGGCTACGTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1200  
Db 1488 GAGGCTACGTGCTACATTTCCAGTGTGTTGTAGTCTCAGCCACAGCTGATTTCTTTT 1547  
Qy 1201 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260  
Db 1548 GTTGTGTTGGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607  
Qy 1261 GGAGTGTAGGAGAGGGCTGGTATTAGTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1320  
Db 1608 GGAGTGTAGGAGAGGGCTGGTATTAGTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1667  
Qy 1321 ATAGGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATAACAGCACTGAGCC 1380  
Db 1668 ATAGGTAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAGAAATAACAGCACTGAGCC 1727  
Qy 1381 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1420  
Db 1728 CACTCCCTGTCAACCTCGGTGATCGGGAGCAGGGCCAG 1767



Wed Dec 8 12:30:21 2004

us-10-718-264-15.rni

Page 16

Search completed: December 7, 2004, 20:05:45  
Job time : 160 secs

---

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 17:33:09 ; Search time 877 seconds  
(without alignments)  
10576.656 Million cell updates/sec

Title: US-10-718-264-15  
Perfect score: 1767  
Sequence: 1 accagcgacttcggcagc.....agaagtcgctgaagtatt 1767

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1645.6	93.1	1768	2 AAX83754	Aax83754 Porcine c
2	1642.4	92.9	1768	2 AAF75841	Aaf75841 PCV DNA f
3	1636.8	92.6	1768	4 AAF75840	Aaf75840 PCV DNA f
4	1620	91.7	1768	8 ABV72527	Abv72527 Nucleotid
5	1545.4	87.5	1786	2 AAX83755	Aax83755 Porcine c
6	1412	79.9	1767	2 AAX35378	Aax35378 Nucleotid
7	1412	79.9	1767	2 AAX35210	Aax35210 Nucleotid
8	1412	79.9	1767	3 AAZ56869	Aaz56869 DNA seque
9	1412	79.9	1767	3 AAF75835	Aaf75835 PCV DNA f
10	1410.4	79.8	1767	2 AAX35379	Aax35379 Nucleotid
11	1410.4	79.8	1767	2 AAX35211	Aax35211 Nucleotid
12	1410.4	79.8	1767	3 AAZ56870	Aaz56870 DNA seque
13	1410.4	79.8	1767	4 AAF75836	Aaf75836 PCV DNA f
14	1335.4	75.6	1768	2 AAX35381	Aax35381 Nucleotid
15	1335.4	75.6	1768	2 AAX35380	Aax35380 Nucleotid
16	1335.4	75.6	1768	2 AAX35213	Aax35213 Nucleotid
17	1335.4	75.6	1768	2 AAX35212	Aax35212 Nucleotid
18	1335.4	75.6	1768	3 AAZ56871	Aaz56871 DNA seque
19	1335.4	75.6	1768	3 AAZ56872	Aaz56872 DNA seque
20	1335.4	75.6	1768	4 AAF75837	Aaf75837 PCV DNA f
21	1335.4	75.6	1768	4 AAF75838	Aaf75838 PCV DNA f

22	1324.6	75.0	1768	2 AAX35382	Aax35382 Nucleotid
23	1324.6	75.0	1768	2 AAX35012	Aax35012 Genomic D
24	1324.6	75.0	1768	2 AAX35214	Aax35214 Nucleotid
c	25	1176.4	66.6	1768	9 AAL57176 Porcine c
	26	1144.4	64.8	1361	2 AAX83757 Porcine c
	27	1005.6	56.9	1759	2 AAX85593 Nucleotid
	28	1000.8	56.6	1759	2 AAX87992 Porcine c
	29	920.8	52.1	3609	4 AAF28320 Nucleotid
c	30	890.6	50.4	1759	2 AAX35013 Nucleotid
	31	886.4	50.2	1759	4 AAF75839 DNA fragm
	32	866.4	49.0	1768	6 AAX08205 PMWS-Porc
	33	864.8	48.9	1768	6 AAX08207 CT-Porcine
	34	863.2	48.9	1768	6 AAX08206 PMWS-Porc
	35	863.2	48.9	1768	6 AAX08204 PMWS-Porc
	36	860	48.7	1768	6 AAX08203 PMWS-Porc
	37	856.8	48.5	1774	6 AAX08219 PMWS-Porc
	38	841.2	47.6	1762	6 AAX08202 PMWS-Porc
	39	741.8	42.0	5285	4 AAH74865 Nucleotid
	40	741.8	42.0	5285	8 AAX94355 Rolling c
	41	741.8	42.0	5650	4 AAH74866 Nucleotid
	42	741.8	42.0	5650	8 AAX94356 Rolling c
	43	719.4	40.7	7460	4 AAH74867 Nucleotid
	44	719.4	40.7	7460	8 AAX94361 Rolling c
c	45	674.8	38.2	1773	9 AAL57177 Porcine c

ALIGNMENTS

RESULT 1

AAX83754  
ID AAX83754 standard; DNA; 1768 BP.

AC AAX83754;

DT 27-AUG-1999 (first entry)

DE Porcine circovirus type II 412 nucleotide sequence.

KW Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;  
KW postweaning multisystemic wasting syndrome virus; diagnosis; ds.

OS Porcine circovirus.

PN WO9929717-A2.

PD 17-JUN-1999.

PF 11-DEC-1998; 98WO-CA001130.

PR 11-DEC-1997; 97US-0069233P.

PR 16-DEC-1997; 97US-0069750P.

XX (UWSA-) UNIV SASKATCHEWAN.

XX Wang L, Babiuk LA, Potter AA, Willson P;

XX WPI; 1999-394957/33.

XX New isolated porcine circovirus Type II.

XX Claim 1; Fig 2; 82pp; English.

CC The present invention describes a new isolated porcine circovirus Type II (PCVII), obtained from postweaning multisystemic wasting syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences. AAX24929 to AAX24934 represent PCVII open reading frame (ORF) proteins (N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D). The PCVII polypeptides can be used for treating or preventing PCVII infection in vertebrates. The products can also be used to detect the PCVII

SQ Sequence 1768 BP; 454 A; 361 C; 492 G; 461 T; 0 U; 0 Other;

Query Match		93.1%;	Score 1645.6;	DB 2;	Length 1768;
Best Local Similarity		96.0%;	Pred. No. 0;		
Matches 1698;		Conservative	0;	Mismatches	69;
				Indels	1;
				Gaps	1;
Qy	1	ACGAGCCACTTCGGCAGCGCAGCAGCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	60		
Db	1	ACGAGCCACTTCGGCAGCGCAGCAGCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	60		
Qy	61	AGAAAGATGGAAGAGCGGAGCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC	120		
Db	61	AGAAAGATGGAAGAGCGGAGCCCAACCCCAATAAAAGGTGGGTGTTCACTCTGAATAATC	120		
Qy	121	CTTCGAGAGCAGCGCAAGAAATACGGGATCTCCCAATATCCCTATTTGATATTTTA	180		
Db	121	CTTCGAGAGCAGCGCAAGAAATACGGGAGCTCCCAATCTCCCTATTTGATATTTTA	180		
Qy	181	TTGTTGGCGAGGAGGTAAATGAGGAGGAGCAACACCTCACCTCCAGGGGTTCCTAATT	240		
Db	181	TTGTTGGCGAGGAGGTAAATGAGGAGGAGCAACACCTCACCTCCAGGGGTTCCTAATT	240		
Qy	241	TTGTGAAGAGCAGACTTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG	300		
Db	241	TTGTGAAGAGCAGACTTTTAAATGAAGTGAAGTGGTATTTGGGTGCCCGTGCACATCG	300		
Qy	301	AGAAAGCGAAAGGAGCAGATCAGCAGATAAAGATATCTGCACTAAGAGGCAACTTAC	360		
Db	301	AGAAAGCGAAAGGAGCAGATCAGCAGATAAAGATATCTGCACTAAGAGGCAACTTAC	360		
Qy	361	TGATGGAGTGTGAGCTCTAGATCTCAGGAGCAACGAGTGACCTGTCTACTCTGTGA	420		
Db	361	TTATTTGAATGTGAGCTCTCGATCTCAAGGACAGGAGTGACCTGTCTACTCTGTGA	420		
Qy	421	GTACCTTGTGTGAGAGCGGAGTCTGGTGAACGTTGACAGAGCAGCCTGTACGTTTG	480		
Db	421	GTACCTTGTGTGAGAGCGGAGTCTGGTGAACGTTGACAGAGCAGCCTGTACGTTTG	480		
Qy	481	TCGAAATTTCCGGCGGTGGCTGAATCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGA	540		
Db	481	TCGAAATTTCCGGCGGTGGCTGAATCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGA	540		
Qy	541	ATTGGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAAAATGG	600		
Db	541	ATTGGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGGTAAAGCAAAATGG	600		
Qy	601	CTGCTAAATTTGAGACCCGGAACCAATCTGAAACCCACTAGAACCAAGTGGTGGG	660		
Db	601	CTGCTAAATTTGAGACCCGGAACCAATCTGAAACCCACTAGAACCAAGTGGTGGG	660		
Qy	661	ATGGTTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720		
Db	661	ATGGTTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720		
Qy	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGAGACTTAAAGGTGAACCTG	780		
Db	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGAGACTTAAAGGTGAACCTG	780		
Qy	781	TACCTTTTGGCCCGCAGTATCTGATTCAGGCAATCAGACCCGCTTGGAAATGTACT	840		
Db	781	TACCTTTTGGCCCGCAGTATCTGATTCAGGCAATCAGACCCGCTTGGAAATGTACT	840		
Qy	841	CCTCAACTGTGTGCCCGCAGTATCTGATTCAGGCAATCAGACCCGCTTGGAAATGTACT	900		
Db	841	CCTCAACTGTGTGCCCGCAGTATCTGATTCAGGCAATCAGACCCGCTTGGAAATGTACT	900		
Qy	901	GGAAGAAATGCTACAGAAACCAATCCAGGAGAGGGGGCAGTTCGTACCCCTTCCCCC	960		
Db	901	GGAAGAAATGCTACAGAAACCAATCCAGGAGAGGGGGCAGTTCGTACCCCTTCCCCC	960		
Qy	961	CATGCCCTGAAATTTCCATATGAATAAATTTACTGAGTCTTTTATCACTTCGTATGGT	1020		
Db	961	CATGCCCTGAAATTTCCATATGAATAAATTTACTGAGTCTTTTATCACTTCGTATGGT	1020		

Qy	1021	TTTTATTATTCAATTAAGGGTT-AAAGTGGGGGTCTTTAAAAATTAATTTCTCTGAATTGTA	1079
Db	1021	TTTTATTATTCAATTAAGGGTTCAAGTGGGGGTCTTTAAAGATTAAATTTCTCTGAATTGTA	1080
Qy	1080	CATACATGTTACACGGATATTGTTCTCGTGTATATCTGTTTTCGAAACGAGTGC	1139
Db	1081	CATACATGTTACACGGATATTGTTAGTCTCGTGTATATCTGTTTTCGAAACGAGTGC	1140
Qy	1140	CGAGCCCTACGTTGCTATCTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGTTTCTTT	1199
Db	1141	CGAGCCCTACGTTGCTTCCATTTCCAGAGTTTGTAGCTCAGCCAAAGCTGATTTCTTT	1200
Qy	1200	TGTTGTTGGTGGAGTAATCAATAGTGAATCTAGACAGGTTTGGGGTAAAGTACC	1259
Db	1201	TGTTATTTGGTGGAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAAC	1260
Qy	1260	GGAGTGTAGAGAGGGCTGGTGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGT	1319
Db	1261	GGAGTGTAGAGAGGGTGGGGATTTGTTATGCGGGAGGAGTAGTTTACATATGGGT	1320
Qy	1320	CATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTTATCATCTAAAAATAACAGCAGTGGAGC	1379
Db	1321	CATAGTGAAGGCTGTGGCTTTGTTTACAAAGTTTATCATCTAAAAATAACAGCAGTGGAGC	1380
Qy	1380	CCACTCCCTGTACCTGGGTGATCGGGAGCAGGCGGAGGAGTTCACACCTTAACTTTC	1439
Db	1381	CCACTCCCTGTACCTGGGTGATCGGGAGGAGGAGGAGGAGGAGTTCACACCTTAACTTTC	1440
Qy	1440	TTATTTCTGTAGTATTTCAAGAGGACAGAGCGGGGTTTTCACCCCTCTCTGGGGAGAA	1499
Db	1441	TTATTTCTGTAGTATTTCAAGAGGATAGAGATTTTGTGTCTCCCTCTCCGGGGAGAA	1500
Qy	1500	AGTCATTAATTAATTAATCTCATCATGTCCACCCGAGAGGGGCTTGTGACTGTGGTAC	1559
Db	1501	AGTCGTCATTTTAAATCTCATCATGTCCACCGCCAGAGGGGCTTGTGACTGTGGTAC	1560
Qy	1560	GCTTGACAGTATATCCAGAGTCCGAGAGGGGCTTGAAGATGCCATTTTCTCTTC	1619
Db	1561	GCTTGACAGTATATCCAGAGTCCGAGAGGGGCTTGAAGATGCCATTTTCTCTTC	1620
Qy	1620	TCCAGCGGTAAACGGTGGCGGGGTGACAGAGCCAGGGGGCGGCGGAGGATCTGCCAA	1679
Db	1621	TCCAAACGTTAGCGGTGGCGGGGTGACAGAGCCAGGGGGCGGAGGATCTGCCAA	1680
Qy	1680	GATGGCTGCGGGGGCGGTGCTTCTTTCGCTAACCCCTCTTGGATAGCTATCTG	1739
Db	1681	GATGGCTGCGGGGGCGGTGCTTCTTCTGCGGTAAACCCCTCTTGGATAGCTATCTG	1740
Qy	1740	AAAAACGAAAGTGGCTGTAAAGTATT	1767
Db	1741	AAAAACGAAAGTGGCTGTAAAGTATT	1768

RESULT 2  
AAAF75841  
ID AAF75841 standard; DNA; 1768 BP.  
AC AAF75841;  
XX  
DT 06-AUG-2003 (revised)  
DT 18-MAY-2001 (first entry)  
XX  
DE PCV DNA fragment of Imp 1121 strain.  
XX  
KW Vaccine; pig; myocarditis; abortion; intrauterine infection;  
KW multisystemic wasting syndrome; ds.  
XX  
OS Porcine circovirus type 2.  
XX  
FN WO200116330-A2.  
XX  
PD 08-MAR-2001.

PF 28-AUG-2000; 2000WO-EP008781.  
XX  
PR 31-AUG-1999; 99US-0151564P.  
PR 31-MAY-2000; 2000US-00583350.  
XX  
XX (MERI-) MERIAL.  
PA (UYSA-) UNIV SASKATCHEWAN.  
PA (UYBE-) UNIV QUEBENS BELFAST.  
XX  
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CB, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;  
XX  
DR WPI; 2001-244408/25.  
XX  
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition  
PT to treat pigs against myocarditis, abortion, intrauterine infection  
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-  
PT 2.  
XX  
XX Claim 11; Fig 7; 134pp; English.  
XX  
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)  
CC immunogen to formulate a vaccine composition to prevent or treat pigs  
CC against myocarditis and/or abortion and/or intrauterine infection and/or  
CC post-weaning, multisystemic wasting syndrome and other pathological  
CC sequelae associated with PCV-2. The present sequence is a DNA fragment  
CC of a strain of PCV, which was used in the present invention. (Updated on 06-  
CC AUG-2003 to correct OS field.)  
XX  
XX Sequence 1768 BP; 452 A; 359 C; 496 G; 461 T; 0 U; 0 Other;  
SQ

Query Match 92.9%; Score 1642.4; DB 4; Length 1768;  
Best Local Similarity 95.9%; Pred. No. 0;  
Matches 1696; Conservative 0; Mismatches 71; Indels 1; Gaps 1;

QY 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
DB 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTCTCACTCTGAATAATC 120  
DB 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTCTCACTCTGAATAATC 120  
QY 121 CTTCCGAGACGAGCGCAAGAAATACGGATCTTCCATATCCCTATTTGATTTTAA 180  
DB 121 CTTCCGAGACGAGCGCAAGAAATACGGAGCTCCCAATCTCCCTATTTGATTTTAA 180  
QY 181 TTGTTGGCGAGGAGGTATAGGAGGAGCAACACCTCACCTCCAGGGGTTTCGCTAAT 240  
DB 181 TTGTTGGCGAGGAGGTATAGGAGGAGCAACACCTCACCTCCAGGGGTTTCGCTAAT 240  
QY 241 TTGTGAAGAGCAGACTTTTAAATGAAGTGGTATTTGGGTGCCCGTCCCAATCG 300  
DB 241 TTGTGAAGAGCAAACTTTTAAATGAAGTGGTATTTGGGTGCCCGTCCCAATCG 300  
QY 301 AGAAGCGAAGAAACAGATCAGCAGATAAGAAATATCGCAGTAAGAGGCAACTTAC 360  
DB 301 AGAAGCGAAGAACTGATCAGCAGATAAGAAATATTTGCAATAAAGAGGCAACTTAC 360  
QY 361 TGATGAGGTGGAGCTCTAGATCTCAGGCAACCGAGTGACCTGTCTACTGTGTGA 420  
DB 361 TTATTGAATGTGAGCTCTCGATCTCAAGGACACGAGTGACCTGTCTACTGTGTGA 420  
QY 421 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTCAGAGCAGCAACCTGTAAAGTTG 480  
DB 421 GTACCTTTGTTGAGAGCGGAGTCTGGTGACCGTTCAGAGCAGCAACCTGTAAAGTTG 480  
QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCGAGAGCGTG 540  
DB 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATGCGAGAGCGTG 540  
QY 541 ATTGGAAGACTAATGTACAGCTATTGTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600

Db 541 ATTGGAAGACCAATGTACAGCTATTGTTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600  
QY 601 CTGCTAATTTTGCAGACCCCGAAACACACATACTGGAAACACACCTAGAAAACAAGTGGTGG 660  
Db 601 CTGCTAATTTTGCAGACCCCGAAACACACATACTGGAAACACACCTAGAAAACAAGTGGTGG 660  
QY 661 ATGGTTACCATGTGTGAAGAGTGGTGTATTTGATGATCTTTTATGGCTGGCTGCCCTGGG 720  
Db 661 ATGGTTACCATGTGTGAAGAGTGGTGTATTTGATGATCTTTTATGGCTGGCTGCCCTGGG 720  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGAGACTAAAGGTGGAACCTG 780  
Db 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGAGACTAAAGGTGGAACCTG 780  
QY 781 TACCTTTTGGCCCGCAGTATTCTGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840  
Db 781 TACCTTTTGGCCCGCAGTATTCTGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840  
QY 841 CCTCAACTGTGTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTTCTTGGTATTTT 900  
Db 841 CCTCAACTGTGTCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTTCTTGGTATTTT 900  
QY 901 GGAAGATGCTACAGAAACATCCACGAGGAGGGGCCAGCTTCTCACCCCTTTCCCCCC 960  
Db 901 GGAAGATGCTACAGAAACATCCACGAGGAGGGGCCAGCTTCTCACCCCTTTCCCCCC 960  
QY 961 CATCCCTGGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020  
Db 961 CATCCCTGGAATTTCCATATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020  
QY 1021 TTTTATTATTCA - TTTAAGGTTAAGTGGGGTCTTTAAATAAATAAATCTCTGAATTTGA 1079  
Db 1021 TTTTATTATTCA TTTAAGGTTAAGTGGGGTCTTTAAGATTAATAATCTCTGAATTTGA 1080  
QY 1080 CATACATGTTTACAGGATTTGATTTCTCTGGTGTATATATCTGTTTTCGACGAGTGC 1139  
Db 1081 CATACATGTTTACAGGATTTGATTTCTCTGGTGTATATCTGTTTTCGACGAGTGC 1140  
QY 1140 CGAGGCTTACGTTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACACAGCTGTTTCTTT 1199  
Db 1141 CGAGGCTTACGTTGGTCTACATTTCTAGAGTTTGTAGCTCAGCCAAAGCTGATTCCTTT 1200  
QY 1200 TGTGTTTGGTGGAAAGTAATCAATAGTGAATCTAGACAGGTTTGGGGTGAAGTACC 1259  
Db 1201 TGTGTTTGGTGGAAAGTAATCAATAGTGGAGTCAAGAACAGGTTGGGTGTGAAGTAA 1260  
QY 1260 GGGAGTGTAGAGAGGGCTGGTATGTTATGCGGAGGAGTGTATACATAGGGGT 1319  
Db 1261 GGGAGTGTAGAGAGGGTGGGGATTTGATGCGGAGGAGTGTATACATATGGGT 1320  
QY 1320 CATAGTGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAAAATAACAGCACTGGAGC 1379  
Db 1321 CATAGTGTAGGGCTGTGGCTTTGTTACAAAGTTATCATCTAGAATAACAGCACTGGAGC 1380  
QY 1380 CCACTCCCTGTGACCCCTGGGTGATCGGGAGCAGGGCCAGAAATCAACCTTAACTTTTC 1439  
Db 1381 CCACTCCCTGTGACCCCTGGGTGATCGGGAGCAGGGCCAGAAATCAACCTTAACTTTTC 1440  
QY 1440 TTATCTGTAGTATTTCAAAGGCAAGAGCGGGGTTTGAACCCCTCTCTGGGGAGAA 1499  
Db 1441 TTATCTGTAGTATTTCAAAGGCAAGAGCGGGTATTTGTTGGTCTCCCGGGGAGCA 1500  
QY 1500 AGTCATTAATTTGAATCTCATCATGTCACCCCGCAGGAGGGCGTTCTGACTGTGGTTC 1559  
Db 1501 AGTCGTCAATTTTAAATCTCATCATGTCACCCCGCAGGAGGGCGTTGTGACTGTAGTAC 1560  
QY 1560 GCTTGACAGTATATCCGAGGTGCGGGAGGAGCGGGTGTGAAGATGCCATTTTCTCTTC 1619  
Db 1561 GCTTGACAGTATATCCGAGGTGCGGGAGGAGCGGGTGTGAAGATGCCATTTTCTCTTC 1620  
QY 1620 TCCAGCGGTAAACGTTGGCGGGGTGGAACGAGCAGGGCGGGCGGAGGATCTGCGCAA 1679  
Db 1620 TCCAGCGGTAAACGTTGGCGGGGTGGAACGAGCAGGGCGGGCGGAGGATCTGCGCAA 1679

Db	1621	TCCAACGGTAGCGGTGGCGGGGTGGACGAGCCAGGGCGGGCGGAGGATCTGGCCAA	1680
Qy	1680	GATGGCTGGCGGGCGGGTGTCTTCTTCTCGGTAAACGCCCTCCTTGGATACGTATATCTG	1739
Db	1681	GATGGCTGGCGGGCGGGTGTCTTCTTCTCGGTAAACGCCCTCCTTGGATACGTATATCTG	1740
Qy	1740	AAAAAGAAAGAGTGGCGCTGTAAGTATT	1767
Db	1741	AAAAAGAAAGAGTGGCGCTGTAAGTATT	1768
RESULT 3			
ID	AAF75840	AAF75840 standard; DNA; 1768 BP.	
XX	AC	AAF75840;	
XX	XX	06-AUG-2003 (revised)	
DT	DT	18-MAY-2001 (first entry)	
XX	DE	PCV DNA fragment of Imp 1103 strain.	
XX	XX	Vaccine; pig; myocarditis; abortion; intrauterine infection;	
KW	KW	multisystemic wasting syndrome; ds.	
XX	OS	Porcine circovirus type 2.	
XX	PN	WO200116330-A2.	
XX	PD	08-MAR-2001.	
XX	PF	28-AUG-2000; 2000WO-EP008781.	
XX	PR	31-AUG-1999; 99US-0151564P.	
XX	PR	31-MAY-2000; 2000US-00583350.	
XX	PA	(MERI-) MERIAL.	
PA	PA	(UYSA-) UNIV SASKATCHEWAN.	
PA	PA	(UYBE-) UNIV QUEENS BELFAST.	
XX	PI	Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Haasard L;	
PI	PI	Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;	
PI	PI	Mcneilly F;	
XX	XX	WPI; 2001-244408/25.	
DR	XX	Use of porcine circovirus-2 immunogen to formulate a vaccine composition	
XX	PT	to treat pigs against myocarditis, abortion, intrauterine infection	
PT	PT	and/or post-weaning, multisystemic wasting syndrome associated with PCV-	
PT	PT	2.	
XX	PS	Claim 10; Fig 6 #2; 134pp; English.	
XX	XX	The present invention relates to the use of porcine circovirus-2 (PCV-2)	
CC	CC	immunogen to formulate a vaccine composition to prevent or treat pigs	
CC	CC	against myocarditis and/or abortion and/or intrauterine infection and/or	
CC	CC	post-weaning, multisystemic wasting syndrome and other pathological	
CC	CC	sequelae associated with PCV-2. The present sequence is a DNA fragment of	
CC	CC	a strain of PCV, which was used in the present invention. (Updated on 06-	
CC	CC	AUG-2003 to correct OS field.)	
XX	XX	Sequence 1768 BP; 450 A; 360 C; 496 G; 460 T; 0 U; 2 Other;	
SQ	XX		
Query Match			
Best Local Similarity 92.6%; Score 1636.8; DB 4; Length 1768;			
Matches 1691; Conservative 2; Mismatches 74; Indels 1; Gaps 1;			
Qy	1	ACCAGCGCACTTCGGCAGCGGCGGACACCTCGGCAGACACCTCAGCAGCAACATGCCAGCA	60
Db	1	ACCAGCGCACTTCGGCAGCGGCGGACACCTCGGCAGACACCTCAGCAGCAACATGCCAGCA	60
Qy	61	AGAAGATGGAAGAGCGGACCCCAACCCCATAAAGGTGGGTTCACCTCTGAATATC	120

Qy	1200	TGTTGTTTGGTTTGGAAAGTAATCAATAGTGAAGTCTAGGACAGGTTTGGGGTAAAGTACC	1259
Dd	1201	TGTTATTTGGTTTGGAAAGTAATCAATAGTGAGTCAAGAACAGCTTTGGGTGTCAAGTAAAC	1260
Qy	1260	GGGAGTGTTAGGAGAAAGGGCTGGGTTATGTGTATGGCGGAGGAGTAGTTAGTTACATAGGGGT	1319
Dd	1261	GGGAGTGTTAGGAGAAAGGGTTGGGGGATTTATATGGCGGAGGAGTAGTTAGTTTACATATGGGT	1320
Qy	1320	CATAGGTGAGGGCTGTGGCCCTTTGTTACAAGTTATCATCTAAATAAACAAGCACTCGAGC	1379
Dd	1321	CATATGTTTGGGCTGTGGCCCTTTGGTACAAGTTATCATCTAGAATAACAGCAGTGGAGC	1380
Qy	1380	CCACTCCCTGTCAACCCCTGGGTGATCGGGAGCAGGGCCAGAAATTCAACTTAACCTTTTC	1439
Dd	1381	CCACTCCCTTATCAACCCCTGGGTGATGGGGAGCAGGGCCAGAAATTCAACTTAACCTTTTC	1440
Qy	1440	TTATTTCTGTAGTATTCAAAGGACACAGAGCGGGGTTTGACCCCTCTCTGGGGGAAGAA	1499
Dd	1441	TTATTTCTGTAGTATTCAAAGGGTATAGAGATTTGTTGGTCCCCCTCCCGGGGAACAA	1500
Qy	1500	AGTCATTAATATTGAATCTCATCATGTCCACCGCCACGAGAGGGGTTCTGACTGTGGTTC	1559
Dd	1501	AGTCGTCAATTTTAAATCTCATCATGTCCACCGCCACGAGAGGGGTTGTGACTGTGGTAC	1560
Qy	1560	GCATTGACATGATATCCGAAGGTCGGGAGAGGGGGTGTGAAGATGCCAATTTTCTCTTC	1619
Dd	1561	GCATTGACAGTATATCCGAAGGTCGGGAGAGGGGGTGTGAAGATGCCAATTTTCTCTTC	1620
Qy	1620	TCCAGCGGTAAACGGTGGCGGGGTGGACGAGCGAGGGCGGGCGGAGGATCTGGGCCAA	1679
Dd	1621	TCCAACCGTTAGCGGTGGCGGGGTGGACGAGCCNAGGGCGGGCGGAGGATCTGGGCCAA	1680
Qy	1680	GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAAACGCCCTCTTGGATACGTATCATCTG	1739
Dd	1681	GATGGCTGCGGGGGCGGTGTCTTCTTCTCGGTAAACGCCCTCTTGGATATGTATAGCTG	1740
Qy	1740	AAAAAGAAAGAGTGGCGCTGTAGTATT	1767
Dd	1741	AAAAAGAAAGAGTGGCGCTGTAGTATT	1768

## RESULT 4

RESOL 4  
ARV72527

ABV72527  
ID ABV72527 standard: DNA: 1768 bp.

XX  
XX  
17037/ANBY

AC ABV72527:

XX  
AC  
ADV 72327,

27-OCT-2003 (revised)

DT	27-OCT-2003	(revised)
DT	29-JAN-2003	(first entry)

XX  
ID 6007-NY-0-62 (TTCB entry)

XX  
NE  
Nucleotide sequence of porcine circovirus

DE NUCLEOTIDE SEQUENCE OF POLY

[illegible]

KW PCV2; mammalian circovirus; virus culture; gene  
yy

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

OS porcine circovirus; 2.

**THE**

FH	Key	Time
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
12	12	12
13	13	13
14	14	14
15	15	15
16	16	16
17	17	17
18	18	18
19	19	19
20	20	20
21	21	21
22	22	22
23	23	23
24	24	24
25	25	25
26	26	26
27	27	27
28	28	28
29	29	29
30	30	30
31	31	31
32	32	32
33	33	33
34	34	34
35	35	35
36	36	36
37	37	37
38	38	38
39	39	39
40	40	40
41	41	41
42	42	42
43	43	43
44	44	44
45	45	45
46	46	46
47	47	47
48	48	48
49	49	49
50	50	50
51	51	51
52	52	52
53	53	53
54	54	54
55	55	55
56	56	56
57	57	57
58	58	58
59	59	59
60	60	60
61	61	61
62	62	62
63	63	63
64	64	64
65	65	65
66	66	66
67	67	67
68	68	68
69	69	69
70	70	70
71	71	71
72	72	72
73	73	73
74	74	74
75	75	75
76	76	76
77	77	77
78	78	78
79	79	79
80	80	80
81	81	81
82	82	82
83	83	83
84	84	84
85	85	85
86	86	86
87	87	87
88	88	88
89	89	89
90	90	90
91	91	91
92	92	92
93	93	93
94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT	CDS
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
9	9
10	10
11	11
12	12
13	13
14	14
15	15
16	16
17	17
18	18
19	19
20	20
21	21
22	22
23	23
24	24
25	25
26	26
27	27
28	28
29	29
30	30
31	31
32	32
33	33
34	34
35	35
36	36
37	37
38	38
39	39
40	40
41	41
42	42
43	43
44	44
45	45
46	46
47	47
48	48
49	49
50	50
51	51
52	52
53	53
54	54
55	55
56	56
57	57
58	58
59	59
60	60
61	61
62	62
63	63
64	64
65	65
66	66
67	67
68	68
69	69
70	70
71	71
72	72
73	73
74	74
75	75
76	76
77	77
78	78
79	79
80	80
81	81
82	82
83	83
84	84
85	85
86	86
87	87
88	88
89	89
90	90
91	91
92	92
93	93
94	94
95	95
96	96
97	97
98	98
99	99
100	100

```
FT
/*tag= a
```

FT /note= "ORF1;"

FT	CDS	complement (10
----	-----	----------------

FT /\*tag= b

FT /note= "ORF2;"

XX

PN WO200277210-A2.

XX

PD 03-OCT-2002.

2000

27-MAR-2002: 2002WO-CA0000413.

1  
4  
4  
5  
5  
4  
4  
3  
  
2  
2  
4  
5  
5  
4  
  
7  
4  
5  
5  
4  
  
2  
2  
2  
2  
2  
4

27-MAR-2001: 2001US-0279173P.

13C/T6/20-COT007 / T002-YFM-12 Y3  
XX

Σ

[illegible]

Db	1691	CATGGCTGGGGGGGGTGTCTTCTTCTGCGGTAAACGCTCCTCTTGGATACGTATAGCTG	1740
Qy	1740	AAAAACGAAGAAGTGCCTCTTAAGTATT	1767
Db	1741	AAAAACGAAGAAGTGCCTCTTAAGTATT	1768
RESULT 5			
AX83755	AX83755 standard; DNA; 1786 BP.		
ID	AX83755	XX	
AX	AX83755;	XX	
AC	AC	XX	
DT	27-AUG-1999 (first entry)	XX	
XX	Porcine circovirus type II 9741 nucleotide sequence.	XX	
DE	Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine;	XX	
KW	postweaning multisystemic wasting syndrome virus; diagnosis; ds.	XX	
KM	Porcine circovirus.	XX	
OS	XX	XX	
XX	WO929717-A2.	XX	
PN	17-JUN-1999.	XX	
XX	11-DEC-1998; 98WO-CA001130.	XX	
XX	11-DEC-1997; 97US-0069233P.	XX	
PR	16-DEC-1997; 97US-0069750P.	XX	
XX	(UYSA-) UNIV SASKATCHEWAN.	XX	
PA	Wang L, Babiuk LA, Potter AA, Willson P;	XX	
PI	WPI; 1999-394957/33.	XX	
DR	New isolated porcine circovirus Type II.	XX	
XX	Claim 1; Fig 4; 82pp; English.	XX	
PS	The present invention describes a new isolated porcine circovirus Type II	XX	
CC	(PCVII), obtained from postweaning multisystemic wasting syndrome-	XX	
CC	affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences.	XX	
CC	AAV24929 to AAV24934 represent PCVII open reading frame (ORF) proteins	XX	
CC	(N.B. the PCVII ORFs given in Fig 2A to Fig 2B do not correspond exactly	XX	
CC	with the PCVII ORFs given in Fig 3A to Fig 3D). The PCVII polypeptides	XX	
CC	can be used for treating or preventing PCVII infection in vertebrates.	XX	
CC	The products can also be used to detect the PCVII	XX	
XX	Sequence 1786 BP; 467 A; 367 C; 481 G; 471 T; 0 U; 0 Other;	XX	
SQ	Query Match 87.5%; Score 1545.4; DB 2; Length 1786;	XX	
	Best Local Similarity 94.3%; Pred. No. 0;	XX	
	Matches 1673; Conservative 0; Mismatches 86; Indels 16; Gaps 6;	XX	
Qy	1	ACCAGCGCACTTCGGCAGCGGACGACCTCGGCGAGCACTCAGCAGCAACATGCCAGCA	60
Db	1	ACCAGCGCACTTCGGCAGCGGACGACCTCGGCGAGCACTCAGCAGCAACATGCCAGCA	60
Qy	61	AGAAGAATGGAAGAAGCGGACCCCAACCCCAATAAAGGTGGGTGTTCACTCTGAATAATC	120
Db	61	AGAAGAATGGAAGAAGCGGACCCCAACCCCAATAAAGGTGGGTGTTCACTCTGAATAATC	120
Qy	121	CTTCCGAGAGCGGCAAGAAAATACGGGATCTTCCCAATATCCCTATTTGATTATTTA	180
Db	121	CTTCCGAGAGCAAGCAAGAAAATACGGGAGCTCCCAATCTCCCTATTTGATTATTTA	180
Qy	181	TTGTTGGCGAGGAGGTAATGAGGAAGCAACACCTCACCTCAGGGGTTCCGCTAATT	240
Db	181	TTGTTGGCGAGGAGGTAATGAGGAAGCAACACCTCACCTCAGGGGTTCCGCTAATT	240
Qy	241	TTGTGAAGAAGCAGACTTTTAAATGAAGTGGTATTTGGGTGCGCGCTGCCACATCG	300







PS Claim 14; Fig 1; 48pp; French.

XX The present sequence represents the nucleotide sequence of PCV isolate  
 CC Impl011-48121. The specification describes a preparation of type II  
 CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
 CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
 CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,  
 CC and vectors that express these polypeptides are all useful in vaccines,  
 CC suitable for administration to adult or young pigs, or to pregnant sows  
 CC (for passive immunization of their offspring). DNA isolated from PCV is  
 CC used for in vivo or in vitro expression of viral polypeptides, also as  
 CC probes or primers for diagnosis in usual hybridization or amplification  
 CC assays. These polypeptides may also be used diagnostically to detect PCV-  
 CC specific antibodies, while antibodies raised against the polypeptides can  
 CC be used to detect antigens, in any usual immunoassay format

XX Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;

Query Match 79.9%; Score 1412; DB 2; Length 1767;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	ACCAGCGCATTCCGCGAGCGGCGAGCACCTCGCGACGACCTCAGCAGCAACATGCCCGCA	60
Db	348	ACCAGCGCATTCCGCGAGCGGCGAGCACCTCGCGACGACCTCAGCAGCAACATGCCCGCA	407
Qy	61	AGAAAGATGGAAGACGCGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	120
Db	408	AGAAAGATGGAAGACGCGACCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC	467
Qy	121	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTTTA	180
Db	468	CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTTTA	527
Qy	181	TTGTGGCGAGGAGGTATAGGAGAGGACGACCACTCACTCAGGGGTTTCGCTAAT	240
Db	528	TTGTGGCGAGGAGGTATAGGAGAGGACGACCACTCACTCAGGGGTTTCGCTAAT	587
Qy	241	TTGTGAGAGCAGACTTTTATTAAGTGAAGTGGTATTGGTGCGCGCTCCACATCG	300
Db	588	TTGTGAGAGCAGACTTTTATTAAGTGAAGTGGTATTGGTGCGCGCTCCACATCG	647
Qy	301	AGAAAGCGAAAGACAGATCAGCAGATAAAGAAATCTGCAGTAAAGAGGCAACTTAC	360
Db	648	AGAAAGCGAAAGACAGATCAGCAGATAAAGAAATCTGCAGTAAAGAGGCAACTTAC	707
Qy	361	TGATGAGTGTGAGGCTCTAGATCTCAGGCAACGAGTGAACCTGTCTACTGTGTGA	420
Db	708	TGATGAGTGTGAGGCTCTAGATCTCAGGCAACGAGTGAACCTGTCTACTGTGTGA	767
Qy	421	GTACCTTTGTGAGAGCGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG	480
Db	768	GTACCTTTGTGAGAGCGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAAAGCTTTG	827
Qy	481	TCAGAAATTTCCCGGGCTGGCTGAATCTTTGAAAGTGAGCGGAAATTCAGAACGCTG	540
Db	828	TCAGAAATTTCCCGGGCTGGCTGAATCTTTGAAAGTGAGCGGAAATTCAGAACGCTG	887
Qy	541	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCACCTGGGTGTGTAAAGCAATGGG	600
Db	888	ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCACCTGGGTGTGTAAAGCAATGGG	947
Qy	601	CTGCTAATTTTGAGACCGGAAACACATCTGGAACACCTAGAAACAGAGTGGTGGG	660
Db	948	CTGCTAATTTTGAGACCGGAAACACATCTGGAACACCTAGAAACAGAGTGGTGGG	1007
Qy	661	ATGGTTACCATGTGGAAGTGGTTGTTATTCATGACTTTTATGCTGCTGCCCTGGG	720
Db	1008	ATGGTTACCATGTGGAAGTGGTTGTTATTCATGACTTTTATGCTGCTGCCCTGGG	1067
Qy	721	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGCTAAAGGTGGAAC	780
Db	1068	ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGCTAAAGGTGGAAC	1127

Qy	781	TACCTTTTGGCCCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAATGGTACT	840
Db	1128	TACCTTTTGGCCCGCAGTATTCTGATTACCAACAATCAGACCCCGTTGGAATGGTACT	1187
Qy	841	CCTCAACTGCTGCTCCAGCTGTAGAAGCTCTTTATCGAGGATTACTTCTTGGTATTTT	900
Db	1188	CCTCAACTGCTGCTCCAGCTGTAGAAGCTCTTTATCGAGGATTACTTCTTGGTATTTT	1247
Qy	901	GGAAAGATGCTTACAGAAACAATCCACGGAGGAGGGGCCAGTTCGTCACTTCCCGCC	960
Db	1248	GGAAAGATGCTTACAGAAACAATCCACGGAGGAGGGGCCAGTTCGTCACTTCCCGCC	1307
Qy	961	CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCACTTCGTAATGGT	1020
Db	1308	CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCACTTCGTAATGGT	1367
Qy	1021	TTTTTATTATTCATTAAGGGTTAAGTGGGGGCTCTTTAAATTTAAATTTCTCTGAATTTGAC	1080
Db	1368	TTTTTATTATTCATTAAGGGTTAAGTGGGGGCTCTTTAAAGATTAAATTTCTCTGAATTTGAC	1427
Qy	1081	ATACATGTTTACACGGATATTGTATTCCTGCTCGTATATCTATCTGTTTCGAAACGCAAGTCC	1140
Db	1428	ATACATGTTTACACGGATATTGTATTCCTGCTCGTATATCTATCTGTTTCGAAACGCAAGTCC	1487
Qy	1141	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT	1200
Db	1488	GAGGCTACGTGGTCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT	1547
Qy	1201	GTCTGTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG	1260
Db	1548	GTCTGTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG	1607
Qy	1261	GGAGTGTGTAGAGAGGGCTGGGTTATGTTATGCGGAGGAGGAGTAGTTTACATAGGGGTC	1320
Db	1608	GGAGTGTGTAGAGAGGGCTGGGTTATGTTATGCGGAGGAGGAGTAGTTTACATAGGGGTC	1667
Qy	1321	ATAGTGAGGGCTGTGGCCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC	1380
Db	1668	ATAGTGAGGGCTGTGGCCTTTGTTTACAAAGTTATCATCTAAATAACAGCACTGGAGCC	1727
Qy	1381	CACCTCCCTGTCACTGGGTGATCGGGAGCAGGGCCAG	1420
Db	1728	CACCTCCCTGTCACTGGGTGATCGGGAGCAGGGCCAG	1767

# RESULT 8

AZ56869  
 ID AZ56869 standard; DNA; 1767 BP.

XX AC AZ56869;

XX DT 25-APR-2000 (first entry)

XX DE DNA sequence of PCV Imp.1011-48121 isolate.

XX KW Antigen; porcine multisystemic wasting syndrome; PMWS; antiviral;

XX KW porcine circovirus; PCV; porcine parvovirus; ppv; vaccination; da.

XX OS Porcine circovirus.

XX PN WO200001409-A2.

XX PD 13-JAN-2000.

XX PF 28-JUN-1999; 99WO-BP004698.

XX PR 06-JUL-1998; 98PR-00008777.

XX PA (MERI-) MERIAL.

XX PA (UYBE-) UNIV QUEENS BELFAST.

XX PA (UYSA-) UNIV SASKATCHEWAN.

XX

PI Allan GM, Meehan BM, Ellis JA, Krakowka GS, Audonnet JF;  
 XX WPI; 2000-182091/16.  
 XX Use of a porcine circovirus antigen and a porcine parvovirus antigen for  
 XX vaccination against porcine multisystemic wasting syndrome.  
 XX Disclosure; Fig 1; 6lpp; English.  
 XX The invention provides a novel antigenic preparation directed against  
 CC porcine multisystemic wasting syndrome (PMWS) that comprises porcine  
 CC circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV  
 CC antigens and PPV antigens can be used for vaccination against PMWS. The  
 CC present sequence represents the DNA sequence of PCV Imp.1011-48121  
 CC isolate  
 XX  
 SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;  
 Query Match 79.9%; Score 1412; DB 3; Length 1767;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 ACCAGCGACATTCGGCAGCGGAGCAGCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 60  
 DB 348 ACCAGCGACATTCGGCAGCGGAGCAGCCTCGCAGCACCTCAGCAGCAACATGCCAGCA 407  
 QY 61 AGAAGAATGGAAGACGGACCCCAACCCCATAAAGTGGTGTCTACTCTGAATAATC 120  
 DB 408 AGAAGAATGGAAGACGGACCCCAACCCCATAAAGTGGTGTCTACTCTGAATAATC 467  
 QY 121 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTATTA 180  
 DB 468 CTTCCGAGACGAGCGCAAGAAATACCGGATCTTCCAAATATCCCTATTTGATTTATTA 527  
 QY 181 TTGTTGGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 240  
 DB 528 TTGTTGGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 587  
 QY 241 TTGTTGAGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 300  
 DB 588 TTGTTGAGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 647  
 QY 301 AGAAGCGAAGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 360  
 DB 648 AGAAGCGAAGGAGGAGGTAAATGAGGAAGGACCAACCTCACCTCAGGGGTTCGCTAATT 707  
 QY 361 TGATGAGGTGTGAGGTCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGTGTA 420  
 DB 708 TGATGAGGTGTGAGGTCTAGATCTCAGGGAACAACGAGTGAACCTGTCTACTGTGTA 767  
 QY 421 GTACCTTTGAGAGCGGGAGTCTGGTGACCGTTGACAGCAGCACCTGTAAAGCTTTG 480  
 DB 768 GTACCTTTGAGAGCGGGAGTCTGGTGACCGTTGACAGCAGCACCTGTAAAGCTTTG 827  
 QY 481 TCAGAAATTTCCGCGGGTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCAAGACGCTG 540  
 DB 828 TCAGAAATTTCCGCGGGTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCAAGACGCTG 887  
 QY 541 ATTGGAAGACTAATGTACAGTCAATTTGTTGGGGCCACCTGGGTGTGTAAGCAATGGG 600  
 DB 888 ATTGGAAGACTAATGTACAGTCAATTTGTTGGGGCCACCTGGGTGTGTAAGCAATGGG 947  
 QY 601 CTGCTAATTTGAGACCGGGAACCAATCTAGGAAACCACTAGAAACCAAGTGGTGGG 660  
 DB 948 CTGCTAATTTGAGACCGGGAACCAATCTAGGAAACCACTAGAAACCAAGTGGTGGG 1007  
 QY 661 ATGGTTACCATGTTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720  
 DB 1008 ATGGTTACCATGTTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
 QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTTAAGTGGGACTG 780  
 DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATGACTTAAGTGGGACTG 1127

QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTTGGAATGGTACT 840  
 DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTACAGCAATCAGACCCCGTTGGAATGGTACT 1187  
 QY 841 CTTCAACTGCTGTCAGCTGTAGAAGCTCTTTATCGGAGGATTAATTCCTTGGTATTTT 900  
 DB 1188 CTTCAACTGCTGTCAGCTGTAGAAGCTCTTTATCGGAGGATTAATTCCTTGGTATTTT 1247  
 QY 901 GGAAGAGTCTACAGCAATCCAGGAGGAAGGGGCGAGTTCGTCAACCTTTTCCCCC 960  
 DB 1248 GGAAGAGTCTACAGCAATCCAGGAGGAAGGGGCGAGTTCGTCAACCTTTTCCCCC 1307  
 QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1020  
 DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTTTATCACTTCGTAATGGT 1367  
 QY 1021 TTTTATTAATTAAGGTTAAGTGGGGGCTTTAAATTAATTAATTTCTCGAATTGTAC 1080  
 DB 1368 TTTTATTAATTAAGGTTAAGTGGGGGCTTTAAAGATTAAATTTCTCGAATTGTAC 1427  
 QY 1081 ATACATGGTTACACGGATATTTCTCTGGTCTGATATATCTGTTTTCGAACGCGAGTGC 1140  
 DB 1428 ATACATGGTTACACGGATATTTCTCTGGTCTGATATATCTGTTTTCGAACGCGAGTGC 1487  
 QY 1141 GAGGCTCTAGTGGTCTTACATTTCCAGCATTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1200  
 DB 1488 GAGGCTCTAGTGGTCTTACATTTCCAGCATTTTGTAGTCTCAGCCACAGCTGTTCTTTT 1547  
 QY 1201 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1260  
 DB 1548 GTTGTGTTGGTGGAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1607  
 QY 1261 GAGTGTAGGAGAGGGCTGAGTATGATGCGGAGGAGTGTAGTATTTACATAGGGGTC 1320  
 DB 1608 GAGTGTAGGAGAGGGCTGAGTATGATGCGGAGGAGTGTAGTATTTACATAGGGGTC 1667  
 QY 1321 ATAGGTGAGGGCTGTGGCTTTGTTTCAAGTTATCATCTAAATTAACAGCACTGAGCC 1380  
 DB 1668 ATAGGTGAGGGCTGTGGCTTTGTTTCAAGTTATCATCTAGAATAACAGCACTGAGCC 1727  
 QY 1381 CACTCCCTGTCAACCTGGGTGATCGGAGCAGGGCCAG 1420  
 DB 1728 CACTCCCTGTCAACCTGGGTGATCGGAGCAGGGCCAG 1767

## RESULT 9

AAF75835  
 ID AAF75835 standard; DNA; 1767 BP.

XX AAF75835;

XX AC  
 XX XX  
 DT 06-AUG-2003 (revised)  
 DT 18-MAY-2001 (first entry)

XX PCV DNA fragment of Imp 1011-48121 strain.

XX Vaccine; pig; myocarditis; abortion; intrauterine infection;  
 XX multisystemic wasting syndrome; ds.

XX Porcine circovirus type 2.

XX WO200116330-A2.

XX 08-MAR-2001.

XX 28-AUG-2000; 2000WO-EP008781.

XX 31-AUG-1999; 99US-0151564P.

XX 31-MAY-2000; 2000US-00583350.

XX (MERI-) MERIAL.

XX (UUSA-) UNIV SASKATCHEWAN.

PA (UYBE-) UNIV QUEENS BELFAST.  
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;  
PI Mcneilly F;  
XX WPI; 2001-244408/25.  
XX  
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition  
PT to treat pigs against myocarditis, abortion, intrauterine infection  
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-  
PT 2.  
XX  
XX Disclosure; Fig 1 #2; 134pp; English.  
XX  
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)  
CC immunogen to formulate a vaccine composition to prevent or treat pigs  
CC against myocarditis and/or abortion and/or intrauterine infection and/or  
CC post-weaning, multisystemic wasting syndrome and other pathological  
CC sequelae associated with PCV-2. The present sequence is a DNA fragment  
CC a strain of PCV, which was used in the present invention. (Updated on 06-  
CC AUG-2003 to correct OS field.)  
XX  
SQ Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;  
Query Match 79.9%; Score 1412; DB 4; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1415; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 1 ACCAGCGCACTTCGGCAGCGGAGCAGCCTCGCAGCACTTCAGCAGCAACATGCCAGCA 60  
DB 348 ACCAGCGCACTTCGGCAGCGGAGCAGCCTCGCAGCACTTCAGCAGCAACATGCCAGCA 407  
QY 61 AGAAGATGGAAGAGCGAGCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC 120  
DB 408 AGAAGATGGAAGAGCGAGCCCAACCCCAATAAAGGTGGGTCTCACTCTGAATAATC 467  
QY 121 CTTCCGACAGCGAGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTTTA 180  
DB 468 CTTCCGACAGCGAGCAAGAAATACGGGATCTTCCAATATCCCTATTGATATTTTA 527  
QY 181 TTGTTGGCAGGAGGTAATAGGAGAGGACGACACCTCACCTCCAGGGGTTTCGTAAT 240  
DB 528 TTGTTGGCAGGAGGTAATAGGAGAGGACGACACCTCACCTCCAGGGGTTTCGTAAT 587  
QY 241 TTGTTGAAGACGACCTTTTAATAAGTGAAGTGAATTTGGTGGCCGCTGCCACATCG 300  
DB 588 TTGTTGAAGACGACCTTTTAATAAGTGAAGTGAATTTGGTGGCCGCTGCCACATCG 647  
QY 301 AGAAGCGAAGAGGACAGATCAGCAATAAAGATACCTGAGTAAAGAGGCACTTAC 360  
DB 648 AGAAGCGAAGAGGACAGATCAGCAATAAAGATACCTGAGTAAAGAGGCACTTAC 707  
QY 361 TGATGGAGTGTGAGCTCCTAGATCTCAGGAGCAACGAGTGAACCTGTCTACTGTGTA 420  
DB 708 TGATGGAGTGTGAGCTCCTAGATCTCAGGAGCAACGAGTGAACCTGTCTACTGTGTA 767  
QY 421 GTACCTTTTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACTCTGAACGTTTG 480  
DB 768 GTACCTTTTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACTCTGAACGTTTG 827  
QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATTCAGAACGCTG 540  
DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAGCGGAAATTCAGAACGCTG 887  
QY 541 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGTGGTGTGTTAAAGCAATGGG 600  
DB 888 ATTGGAAGACTAATGTACAGCTCATTTGTGGGGCCACTGTGGTGTGTTAAAGCAATGGG 947  
QY 601 CTGCTAATTTTGCAGACCGGAAACCAATATCTGGAACCACTAGAAACAAGTGTGGG 660  
DB 948 CTGCTAATTTTGCAGACCGGAAACCAATATCTGGAACCACTAGAAACAAGTGTGGG 1007

QY 661 ATGTTTACCATGTTGAAGAAAGTGGTTTATTTATGATGACTTTTATGGCTGGCTGCCCTGGG 720  
DB 1008 ATGTTTACCATGTTGAAGAAAGTGGTTTATTTATGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACCTG 780  
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACCTG 1127  
QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATACAGACCCCGTTGGAATGGTACT 840  
DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACAGCAATACAGACCCCGTTGGAATGGTACT 1187  
QY 841 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTGTTGTTATTT 900  
DB 1188 CCTCAACTGCTGTCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTGTTGTTATTT 1247  
QY 901 GGAAGATGCTACAGAAACAATCCACGAGGAGGAGGCGCAGTTCGTCAACCTTTTCCCGCC 960  
DB 1248 GGAAGATGCTACAGAAACAATCCACGAGGAGGAGGCGCAGTTCGTCAACCTTTTCCCGCC 1307  
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCTGTAATGGT 1020  
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAAGTCTTTTATCACTTCTGTAATGGT 1367  
QY 1021 TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAATTAATTTCTCTGAATGTAC 1080  
DB 1368 TTTTATTAATTAAGGTTAAGTGGGGGTCTTTAAAGATTAATTTCTCTGAATGTAC 1427  
QY 1081 ATACATGTTTACAGGATATTTGATTCCTGCTGTATATCTGTTTTCGACGAGTGCC 1140  
DB 1428 ATACATGTTTACAGGATATTTGATTCCTGCTGTATATCTGTTTTCGACGAGTGCC 1487  
QY 1141 GAGGCTACGTTGTTTCAATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
DB 1488 GAGGCTACGTTGTTTCAATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCTTTT 1547  
QY 1201 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1260  
DB 1548 GTTGTGTTGGTGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAGTACCG 1607  
QY 1261 GGAGTGTAGGAGAGGCTGGGTTATGTTATGGGAGGAGTGTATACATAGGGGTC 1320  
DB 1608 GGAGTGTAGGAGAGGCTGGGTTATGTTATGGGAGGAGTGTATACATAGGGGTC 1667  
QY 1321 ATAGTGTAGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC 1380  
DB 1668 ATAGTGTAGGCTGTGGCTTTTGTACAAAGTTATCATCTAGATAACAGCACTGGAGCC 1727  
QY 1381 CACTCCCTGTCACTGGGTATCGGGAGCAGGGCCAG 1420  
DB 1728 CACTCCCTGTCACTGGGTATCGGGAGCAGGGCCAG 1767  
RESULT 10  
AA35379  
ID AA35379 standard; DNA; 1767 BP.  
XX  
XX AAX35379;  
XX  
XX 07-JUL-1999 (first entry)  
XX  
XX Nucleotide sequence of PCV isolate Impl011-48285.  
XX  
XX PCV isolate; type II porcine circovirus; PCV; PMWS;  
XX porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
XX Porcine circovirus.  
XX  
XX WO918214-A1.  
XX  
XX 15-APR-1999.  
XX  
XX 01-OCT-1998; 98WO-FR002107.  
XX  
XX PF

XX 03-OCT-1997; 97FR-00012382.  
 PR 22-JAN-1998; 98FR-00000873.  
 PR 20-MAR-1998; 98FR-00003707.  
 XX (MERI-) MERIAL.  
 PA (UYBE-) UNIV QUEBENS BELFAST.  
 PA (UYSA-) UNIV SASKATCHEWAN.  
 XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Haseard L;  
 PI Harding J, Charreyre CE, Chappuis GE;  
 XX WPI; 1999-264024/22.  
 DR New type II porcine circovirus.  
 XX Claim 11; Fig 2; 56pp; French.  
 PS  
 CC The present sequence represents the nucleotide sequence of PCV isolate  
 CC Impl011-48285. The specification describes a preparation of type II  
 CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
 CC from a pig with symptoms of PMWS (porcine multisystemic wasting  
 CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,  
 CC and vectors that express these polypeptides are all useful in vaccines,  
 CC suitable for administration to adult or young pigs, or to pregnant sows  
 CC (for passive immunization of their offspring). DNA isolated from PCV is  
 CC used for in vivo or in vitro expression of viral polypeptides, also as  
 CC probes or primers for diagnosis in usual hybridization or amplification  
 CC assays. These polypeptides may also be used diagnostically to detect PCV.  
 CC specific antibodies, while antibodies raised against the polypeptides can  
 CC be used to detect antigens, in any usual immunoassay format  
 XX  
 SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;

Query Match 79.8%; Score 1410.4; DB 2; Length 1767;  
 Best Local Similarity 99.6%; Pred. No. 0;  
 Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACCAGCGCATTCCGCGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAATGCCAGCA 60  
 DB 348 ACCAGCGCATTCCGCGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAATGCCAGCA 407  
 QY 61 AGAAGATGGAAGAGCGGAGCGCCCAACCCCAATAGAGTGGGTCTCACTCTGTAATATC 120  
 DB 408 AGAAGATGGAAGAGCGGAGCGCCCAACCCCAATAGAGTGGGTCTCACTCTGTAATATC 467  
 QY 121 CTTCCGAGACGAGCGCAAGAAATAACGGGATCTTCCAAATATCCCTATTTGATATTTA 180  
 DB 468 CTTCCGAGACGAGCGCAAGAAATAACGGGATCTTCCAAATATCCCTATTTGATATTTA 527  
 QY 181 TTGTTGGCGAGGAGGTATGAGGAGGAGCAGCCTCAGCAGGAGTTCGCTAATT 240  
 DB 528 TTGTTGGCGAGGAGGTATGAGGAGGAGCAGCCTCAGCAGGAGTTCGCTAATT 587  
 QY 241 TTGTTGAAGAGCAGACTTTTATTAAGTGAAGTGGTATTTGGGTGCCCGCTCCACATCG 300  
 DB 588 TTGTTGAAGAGCAGACTTTTATTAAGTGAAGTGGTATTTGGGTGCCCGCTCCACATCG 647  
 QY 301 AGAAGCGAAGAAAGACAGATCAGCAGAAATAAGATACTGCGAGTAAAGAGGCACTTAC 360  
 DB 648 AGAAGCGAAGAAAGACAGATCAGCAGAAATAAGATACTGCGAGTAAAGAGGCACTTAC 707  
 QY 361 TGAATGAGTGTGAGGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGTGTGA 420  
 DB 708 TGAATGAGTGTGAGGCTCCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGTGTGA 767  
 QY 421 GTACCTTTGTTGAGAGCGGGAGTCTGTGTGACCGCTTGCAGAGCAGCAACCTGTAAACGTTTG 480  
 DB 768 GTACCTTTGTTGAGAGCGGGAGTCTGTGTGACCGCTTGCAGAGCAGCAACCTGTAAACGTTTG 827  
 QY 481 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCGAGAGCGTG 540  
 DB 828 TCAGAAATTTCCCGGGCTGGCTGAACCTTTGAAAGTGAAGCGGAAATGCGAGAGCGTG 887

## RESULT 11

AA35211

ID AA35211 standard; DNA; 1767 BP.

XX AC AA35211;

XX DT 01-JUL-1999 (first entry)

XX DE Nucleotide sequence of PCV isolate Impl011-48285.

XX KW PCV isolate; type II porcine circovirus; PCV; PMWS;

QY 541 ATTGGAAGACTAATGTACACGTCAATGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 600  
 DB 888 ATTGGAAGACTAATGTACACGTCAATGTGGGGCCACCTGGGTGTGTTAAAGCAATGGG 947  
 QY 601 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACCACTAGAAACAAGTGGTGG 660  
 DB 948 CTGCTAAATTTTCAGACCCCGGAAACACATACCTGGAACCACTAGAAACAAGTGGTGG 1007  
 QY 661 ATGGTTACCATGGTGAAGAGTGGTGTATTTATGATGACTTTTATGCTGGCTGCCCTGGG 720  
 DB 1008 ATGGTTACCATGGTGAAGAGTGGTGTATTTATGATGACTTTTATGCTGGCTGCCCTGGG 1067  
 QY 721 ATGATCTACTGAGACCTGTGTGATCCGATATCCATTTGACTGTAGAGACTAAAGTGGAACTG 780  
 DB 1068 ATGATCTACTGAGACCTGTGTGATCCGATATCCATTTGACTGTAGAGACTAAAGTGGAACTG 1127  
 QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTAACGACCAATCAGACCCCGTGGAAATGTACT 840  
 DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTAACGACCAATCAGACCCCGTGGAAATGTACT 1187  
 QY 841 CCTCAACTGTGTCAGCTGTAGAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900  
 DB 1188 CCTCAACTGTGTCAGCTGTAGAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 1247  
 QY 901 GGAAGATGCTACAGAAACAATCCAGGAGGAGGGGCCAGTTTCGTCAACCTTTCCCGCC 960  
 DB 1248 GGAAGATGCTACAGAAACAATCCAGGAGGAGGGGCCAGTTTCGTCAACCTTTCCCGCC 1307  
 QY 961 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCATCTTCGTAATGGT 1020  
 DB 1308 CATGCCCTGAATTTCCATATGAATAAATTAATCTAGTCTTTTATCATCTTCGTAATGGT 1367  
 QY 1021 TTTTATTTATTTAAGGGTTAAGTGGGGGTCTTTAAATTAATTAATTTCTCGAATGTAC 1080  
 DB 1368 TTTTATTTATTTAAGGGTTAAGTGGGGGTCTTTAAGATTAATTTCTCGAATGTAC 1427  
 QY 1081 ATACATGTTTACCGGATATTTGATTCCTGGTCTGATATATCTGTTTCGAACCGAGTGCC 1140  
 DB 1428 ATACATGTTTACCGGATATTTGATTCCTGGTCTGATATATCTGTTTCGAACCGAGTGCC 1487  
 QY 1141 GAGCGCTACGTGTCTACATTTCCAGCAGTTTCTAGTCTCAGCCACAGCTGGTTCTTTT 1200  
 DB 1488 GAGCGCTACGTGTCTACATTTCCAGTGTGTTAGTCTCAGCCACAGCTGATTTCTTTT 1547  
 QY 1201 GTTCTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260  
 DB 1548 GTTCTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607  
 QY 1261 GGAGTGTAGGAGAGCGCTGGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1320  
 DB 1608 GGAGTGTAGGAGAGCGCTGGGTATGTTATGCGGGAGGAGTAGTTTACATAGGGGTC 1667  
 QY 1321 ATAGGTAGGGCTGTGGCTTTGTACAAAGTATCATCTAAATTAACAGCAGCTGGAGCC 1380  
 DB 1668 ATAGGTAGGGCTGTGGCTTTGTACAAAGTATCATCTAAGATTAATTAACAGCAGCTGGAGCC 1727  
 QY 1381 CACTCCCTGTCAACCTGGGTGATCGGGGAGGAGGGCCAG 1420  
 DB 1728 CACTCCCTGTCAACCTGGGTGATCGGGGAGGAGGGCCAG 1767

porcine multisystemic wasting syndrome; pig; vaccine; ss.

XX OS Porcine circovirus.  
XX PN PR2769322-Al.  
XX PD 09-APR-1999.  
XX XX 22-JAN-1998; 98FR-00000873.  
XX PF 03-OCT-1997; 97FR-00012382.  
XX PR (MERI-) MERIAL SAS.  
XX PA Allan G, Meehan B, Clark E, Ellis J, Haines D, Hassard L;  
PI Harding J, Charreyre CE, Chappuis GE;  
XX DR WPI; 1999-246948/21.  
XX XX New type II porcine circovirus, used for, e.g. passive immunization of  
PT pregnant sows.  
XX PS Claim 14; Fig 2; 48pp; French.  
XX CC The present sequence represents the nucleotide sequence of PCV isolate  
CC Imp1011-48285. The specification describes a preparation of type II  
CC porcine circovirus (PCV), which is particularly isolated from a lesion,  
CC from a pig with symptoms of PMS (porcine multisystemic wasting  
CC syndrome). PCV (attenuated or inactivated), polypeptides derived from it,  
CC and vectors that express these polypeptides are all useful in vaccines,  
CC suitable for administration to adult or young pigs, or to pregnant sows  
CC (for passive immunization of their offspring). DNA isolated from PCV is  
CC used for in vivo or in vitro expression of viral polypeptides, also as  
CC probes or primers for diagnosis in usual hybridization or amplification  
CC assays. These polypeptides may also be used diagnostically to detect PCV-  
CC specific antibodies, while antibodies raised against the polypeptides can  
CC be used to detect antigens, in any usual immunoassay format  
XX SQ Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;  
Query Match 79.8%; Score 1410.4; DB 2; Length 1767;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 ACCAGGCACTTCGGCAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 60  
DB 348 ACCAGGCACTTCGGCAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA 407  
QY 61 AGAAGAAATGGAAGAGCGGAGCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 120  
DB 408 AGAAGAAATGGAAGAGCGGAGCCCAACCCCATAAAGGTGGGTGTTCACTCTGAATAATC 467  
QY 121 CTTCCGAAGACGAGCGCAAGAAATAACGGATCTTCCAATATCCCTATTGTAATTTTA 180  
DB 468 CTTCCGAAGACGAGCGCAAGAAATAACGGATCTTCCAATATCCCTATTGTAATTTTA 527  
QY 181 TTGTTGGCAGGAGGTAATGAGAGGAGCAACACCTCACCTCCAGGGGTTTCGCTAAT 240  
DB 528 TTGTTGGCAGGAGGTAATGAGAGGAGCAACACCTCACCTCCAGGGGTTTCGCTAAT 587  
QY 241 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGGTGCCCGTGCACATCG 300  
DB 588 TTGTTGAAGAGCAGACTTTTAAATAAGTGAAGTGGTATTGTTGGGTGCCCGTGCACATCG 647  
QY 301 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAGAGAGGCAACTTAC 360  
DB 648 AGAAGCGAAGGAACAGATCAGCAGAAATAAGAAATCTGCAGTAAGAGAGGCAACTTAC 707  
QY 361 TGATGGAGTGGAGCTCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 420  
DB 708 TGATGGAGTGGAGCTCTAGATCTCAGGAGCAACGGAGTGACCTGTCTACTGCTGTGA 767  
QY 421 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTGTAAACGTTTG 480

DB 768 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTGTAAAGCTTTG 827  
QY 481 TCAGAAATTTCCGGGGCTGGCTGAACTTTTGAAGAGTACGCGGGAATAATCAGAGCGGTG 540  
DB 828 TCAGAAATTTCCGGGGCTGGCTGAACTTTTGAAGAGTACGCGGGAATAATCAGAGCGGTG 887  
QY 541 ATTGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 600  
DB 888 ATTGAAGACTAATGTACACGTCAATTTGGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 947  
QY 601 CTGCTAATTTTGCAGACCCGGAACCAATCTGAAACCACTAGAAACCAAGTGGTGGG 660  
DB 948 CTGCTAATTTTGCAGACCCGGAACCAATCTGAAACCACTAGAAACCAAGTGGTGGG 1007  
QY 661 ATGGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 720  
DB 1008 ATGGTTTACCATGGTGAAGAGTGGTGTATTTGATGACTTTTATGGCTGGCTGCCCTGGG 1067  
QY 721 ATGATCTACTCAGACTGTGTGATCGATATCCATGACTGTGTAGAGACTAAAGTGGAACTG 780  
DB 1068 ATGATCTACTCAGACTGTGTGATCGATATCCATGACTGTGTAGAGACTAAAGTGGAACTG 1127  
QY 781 TACCTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTTGGAATGGTACT 840  
DB 1128 TACCTTTTGGCCCGCAGTATTTCTGATTACCAAGCAATCAGACCCCGTTGGAATGGTACT 1187  
QY 841 CCTCAACTGCTGTCACAGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTTCTTGGTATTTT 900  
DB 1188 CCTCAACTGCTGTCACAGCTGTAGAAAGCTCTTTATCGGAGGATTAATCTTCTTGGTATTTT 1247  
QY 901 GGAAGAAATGCTACAGAAACAATCCACGAGGAGGGGGCAGTTCACCTTTCCCTCC 960  
DB 1248 GGAAGAAATGCTACAGAAACAATCCACGAGGAGGGGGCAGTTCACCTTTCCCTCC 1307  
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAATGCTGTTTATCACTTCTGTAATGGT 1020  
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATGCTGTTTATCACTTCTGTAATGGT 1367  
QY 1021 TTTTATTTTCAATTAAGGTTAAAGTGGGGGCTTTTAAATTAATTAATTTCTGAAATTTGTA 1080  
DB 1368 TTTTATTTTCAATTAAGGTTAAAGTGGGGGCTTTTAAATTAATTTCTGAAATTTGTA 1427  
QY 1081 ATACATGGTTTACAGGATAATTTCTCTGGTGTATATATCTGTTTTCGAAACGAGTGCC 1140  
DB 1428 ATACATGGTTTACAGGATAATTTCTCTGGTGTATATATCTGTTTTCGAAACGAGTGCC 1487  
QY 1141 GAGGCTTACGTGCTTACATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTTT 1200  
DB 1488 GAGGCTTACGTGCTTACATTTTCCAGTATTTGTAGTCTCAGCCACAGCTGATTTCTTTT 1547  
QY 1201 GTTGTGTTGGTTCGAAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260  
DB 1548 GTTGTGTTGGTTCGAAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607  
QY 1261 GGAGTGGTAGGAGAGGGGCTGGGTATGTTATGGTATGGGGGAGGAGTATTTACATAGGGGTC 1320  
DB 1608 GGAGTGGTAGGAGAGGGGCTGGGTATGTTATGGTATGGGGGAGGAGTATTTACATAGGGGTC 1667  
QY 1321 ATAGTGGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAAATTAACAGCACTGGAGCC 1380  
DB 1668 ATAGTGGAGGGCTGTGGCTTTTGTACAAAGTTATCATCTAGAAATTAACAGCACTGGAGCC 1727  
QY 1381 CACTCCCTGTCCACCTGGTGTATCGGGAGCAGGCGCCAG 1420  
DB 1728 CACTCCCTGTCCACCTGGTGTATCGGGAGCAGGCGCCAG 1767

RESULT 12  
AAZ56870  
ID AAZ56870 standard; DNA; 1767 BP.  
XX  
AC AAZ56870;



XX	DT	25-APR-2000 (first entry)	DB	768	GTACCTTGTGGAGAGCGGAGTCTGTGACCGTGTGCAGAGCAGCACCTCTTAACGTTTG	827
XX	DE	DNA sequence of PCV Imp.1011-48285 isolate.	QY	481	TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGCAGCGGAAATTCAGAACGCTG	540
XX	KW	Antigen; porcine multisystemic wasting syndrome; PMWS; antiviral;	DB	828	TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGCAGCGGAAATTCAGAACGCTG	887
XX	KW	porcine circovirus; PCV; porcine parvovirus; PPV; vaccination; ds.	QY	541	ATTGGAAGACTAATGTACACGTCATTGTGGGCCACCTGGGTGTGTAAGAACAAATGGG	600
XX	OS	Porcine circovirus.	DB	888	ATTGGAAGACTAATGTACACGTCATTGTGGGCCACCTGGGTGTGTAAGAACAAATGGG	947
XX	XX	WO200001409-A2.	QY	601	CTGCTAATTTTGCAGACCGCGAAACCACTACTGAAACACCCTAGAAACAGTGGTGG	660
XX	PN	13-JAN-2000.	DB	948	CTGCTAATTTTGCAGACCGCGAAACCACTACTGAAACACCCTAGAAACAGTGGTGG	1007
XX	PD	28-JUN-1999; 99WO-EP004698.	QY	661	ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	720
XX	PF	06-JUL-1998; 98FR-00008777.	DB	1008	ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG	1067
XX	PR	(MERI-) MERIAL.	QY	721	ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAACCTG	780
XX	PA	(UYBE-) UNIV QUEBENS BELFAST.	DB	1068	ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAACCTG	1127
XX	PA	(UYSA-) UNIV SASKATCHEWAN.	QY	781	TACCTTTTGGCCCGCAGTATTTCTGATTTACCGCAATCAGACCCCGTTGGAAATGTACT	840
XX	PI	Allan GM, Meehan BM, Ellis JA, Krakowka GS, Audonnet JF;	DB	1128	TACCTTTTGGCCCGCAGTATTTCTGATTTACCGCAATCAGACCCCGTTGGAAATGTACT	1187
XX	XX	WPI; 2000-182091/16.	QY	841	CTTCAACTGCTGTCGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT	900
XX	DR	Use of a porcine circovirus antigen and a porcine parvovirus antigen for	DB	1188	CTTCAACTGCTGTCGCCAGCTGTAGAAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT	1247
XX	PT	vaccination against porcine multisystemic wasting syndrome.	QY	901	GGAGAAATGCTACAGAAACAATCCAGGAGAGGGGGCAGTTCGTCACCTTCCCGCC	960
XX	PS	Disclosure; Fig 2; 61pp; English.	DB	1248	GGAGAAATGCTACAGAAACAATCCAGGAGAGGGGGCAGTTCGTCACCTTCCCGCC	1307
XX	XX	The invention provides a novel antigenic preparation directed against	QY	961	CATGCCCTGAAATTTCCATATGAAATTAATTTACTGAGTCTTTTATCACTTCGTAATGGT	1020
XX	CC	porcine multisystemic wasting syndrome (PMWS) that comprises porcine	DB	1308	CATGCCCTGAAATTTCCATATGAAATTAATTTACTGAGTCTTTTATCACTTCGTAATGGT	1367
XX	CC	circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV	QY	1021	TTTTTATTTTCAATTAAGGGTTAAGTGGGGGTCTTTAAGATTAATTAATTTCTGAAATGTAC	1080
XX	CC	antigens and PPV antigens can be used for vaccination against PMWS. The	DB	1368	TTTTTATTTTCAATTAAGGGTTAAGTGGGGGTCTTTAAGATTAATTAATTTCTGAAATGTAC	1427
XX	CC	present sequence represents the DNA sequence of PCV Imp.1011-48285	QY	1081	ATACATGTTTACAGGATATTTGATTTCTCGTGTATATCTGTTTTCGAAACGAGTGCC	1140
XX	CC	isolate	DB	1428	ATACATGTTTACAGGATATTTGATTTCTCGTGTATATCTGTTTTCGAAACGAGTGCC	1487
XX	XX	Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;	QY	1141	GAGCCCTACGTTGTTTCACTATTTCCAGCAGTTCAGTCTCAGCCACAGCTGGTTCTTTT	1200
XX	SQ	Query Match 79.8%; Score 1410.4; DB 3; Length 1767;	DB	1488	GAGCCCTACGTTGTTTCACTATTTCCAGCAGTTCAGTCTCAGCCACAGCTGATTTCTTTT	1547
		Best Local Similarity 99.6%; Pred. No. 0;	QY	1201	GTTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG	1260
		Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	DB	1548	GTTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACCG	1607
QY	1	ACCAGGCACTTCGCGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	QY	1261	GGAGTGTAGAGAGGGCTGGGTATGGTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGTC	1320
DB	348	ACCAGGCACTTCGCGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	DB	1608	GGAGTGTAGAGAGGGCTGGGTATGGTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGTC	1667
QY	61	AGAGAAATGGAAGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	QY	1321	ATAGTGTAGGGCTGTGGCCCTTTGTTTACAAAGTTATCATCTTAAATAAACAGCAGCTGGAGCC	1380
DB	408	AGAGAAATGGAAGAGCGGAGCAGCCTCGGAGCAGCCTCAGCAGCAACATGCCAGCA	DB	1668	ATAGTGTAGGGCTGTGGCCCTTTGTTTACAAAGTTATCATCTTAAATAAACAGCAGCTGGAGCC	1727
QY	121	CTTCCGAGACGAGCGCAAGAAATAACGGATCTTCCAAATATCCCTATTTGATTTTGA	QY	1381	CACCTCCCTGTCAACCTGGGTGATCGGGGAGCAGGGCCAG	1420
DB	468	CTTCCGAGACGAGCGCAAGAAATAACGGATCTTCCAAATATCCCTATTTGATTTTGA	DB	1728	CACCTCCCTGTCAACCTGGGTGATCGGGGAGCAGGGCCAG	1767
QY	181	TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACCTCAGCTCCAGGGGTTTCGTAAT				
DB	528	TTGTTGGCGAGGAGGTAATGAGGAGGAGCAACCTCAGCTCCAGGGGTTTCGTAAT				
QY	241	TTGTTGAAGAGCAGACTTTTATTAAGTGAAGTGGTATTTGGGTGCCCGCTGCCAATCG				
DB	588	TTGTTGAAGAGCAGACTTTTATTAAGTGAAGTGGTATTTGGGTGCCCGCTGCCAATCG				
QY	301	AGAAAGCGAAGGAAACAGATCAGCAGAAATAAGAACTAGCAGTAAGAGGCACTTAC				
DB	648	AGAAAGCGAAGGAAACAGATCAGCAGAAATAAGAACTAGCAGTAAGAGGCACTTAC				
QY	361	TGATGAGTGTGGAGTCTCTAGATCTCAGGCAACAGGAGTGACCTGTCTACTGTGTGA				
DB	708	TGATGAGTGTGGAGTCTCTAGATCTCAGGCAACAGGAGTGACCTGTCTACTGTGTGA				
QY	421	GTACCTTGTGGAGAGCGGAGTCTGTGTGACCGTGTGAGAGCAGCAACCTGTAAACGTTG				

RESULT 13  
AAF75836  
ID AAF75836 standard; DNA; 1767 BP.  
XX  
AC AAF75836;

```
XX 06-AUG-2003 (revised)
DT 18-MAY-2001 (first entry)
XX PCV DNA fragment of Imp 1011-48285 strain.
DE Vaccine; pig; myocarditis; abortion; intrauterine infection;
KW multisystemic wasting syndrome; ds.
XX Porcine circovirus type 2.
OS WO200116330-A2.
XX 08-MAR-2001.
XX 28-AUG-2000; 2000WO-EP008781.
XX 31-AUG-1999; 99US-0151564P.
XX 31-MAY-2000; 2000US-00583350.
XX (MERI-) MERIAL.
XX (UYSA-) UNIV SASKATCHEWAN.
XX (UYBE-) UNIV QUEENS BELFAST.
XX Ellis JA, Allan GM, Meehan B, Clark E, Haines D, Hassard L;
PI Harding J, Charreyre CE, Chappuis GE, Krakowka GS, Audonnet JF;
PI Mcneilly F;
XX WPI; 2001-244408/25.
XX Use of porcine circovirus-2 immunogen to formulate a vaccine composition
PT to treat pigs against myocarditis, abortion, intrauterine infection
PT and/or post-weaning, multisystemic wasting syndrome associated with PCV-
PT 2.
XX Disclosure; Fig 2 #2; 134pp; English.
XX The present invention relates to the use of porcine circovirus-2 (PCV-2)
CC immunogen to formulate a vaccine composition to prevent or treat pigs
CC against myocarditis and/or abortion and/or intrauterine infection and/or
CC post-weaning, multisystemic wasting syndrome and other pathological
CC sequelae associated with PCV-2. The present sequence is a DNA fragment of
CC a strain of PCV, which was used in the present invention. (Updated on 06-
CC AUG-2003 to correct OS field.)
XX
XX Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;
Query Match 79.8%; Score 1410.4; DB 4; Length 1767;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 ACCAGGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCAGCA 60
DB 348 ACCAGGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCAGCA 407
QY 61 AGAAGATGGAAGAGCGGACCCCAACCCATAAAGGTGGGTTCACCTCTGAAATAATC 120
DB 408 AGAAGATGGAAGAGCGGACCCCAACCCATAAAGGTGGGTTCACCTCTGAAATAATC 467
QY 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTTATTTA 180
DB 468 CTTCCGAGACGAGCGCAGAAATACGGGATCTTCCAATATCCCTATTGATTTATTTA 527
QY 181 TTCTTGGCGAGGAGGTATAGGAAGGAGCAACACCTACCTCCAGGGGTTTCGCTAAAT 240
DB 528 TTCTTGGCGAGGAGGTATAGGAAGGAGCAACACCTACCTCCAGGGGTTTCGCTAAAT 587
QY 241 TTCTGAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGTGGCCGCTGCCACATCG 300
DB 588 TTCTGAGAGCAGACTTTTAATAAGTGAAGTGTATTTGGTGGCCGCTGCCACATCG 647
QY 301 AGAAAGCGAAGGAAACAGATCAGCAATAAAGAAATCTCAGTAAAGAGGCAACTTAC 360
DB 648 AGAAAGCGAAGGAAACAGATCAGCAATAAAGAAATCTCAGTAAAGAGGCAACTTAC 707
QY 361 TGATGGAGTGTGGAGCTCTAGATCTCAGGACAACCGAGTGACTGTCTACTGTGTGA 420
DB 708 TGATGGAGTGTGGAGCTCTAGATCTCAGGACAACCGAGTGACTGTCTACTGTGTGA 767
QY 421 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTCTAAGCTTTG 480
DB 768 GTACCTTGTGGAGAGCGGAGTCTGTGACCGTTGCAGAGCAGCACCCTCTAAGCTTTG 827
QY 481 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAGCGGGAATAATCAGAAAGCGTG 540
DB 828 TCAGAAATTTCCGCGGCTGCTGAACTTTTGAAGTGAGCGGGAATAATCAGAAAGCGTG 887
QY 541 ATTGGAAGACTAATGTACACGTCATTTGCGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 600
DB 888 ATTGGAAGACTAATGTACACGTCATTTGCGGGCCACCTGGGTGTGTTAAAGCAAAATGGG 947
QY 601 CTGCTAATTTTGCAGACCCGGAACCATATCTGGAACCCACTAGAAACAGTGGTGGG 660
DB 948 CTGCTAATTTTGCAGACCCGGAACCATATCTGGAACCCACTAGAAACAGTGGTGGG 1007
QY 661 ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 720
DB 1008 ATGGTTACCATGTTGAAGAGTGGTGTATTGATGACTTTTATGGCTGGCTGCCCTGGG 1067
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAAC 780
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATGACTGTAGAGACTAAAGGTGGAAC 1127
QY 781 TACCTTTTGGCCCGCAGATTTCTGATATCCAGCAATCAGACCCTGGTGGATGGTACT 840
DB 1128 TACCTTTTGGCCCGCAGATTTCTGATATCCAGCAATCAGACCCTGGTGGATGGTACT 1187
QY 841 CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 900
DB 1188 CCTCAACTGCTGCCAGCTGTAGAGCTCTTTATCGGAGGATTAATCTCTTGGTATTTT 1247
QY 901 GGAAGATGCTACAGAACAAATCCAGGAGGAGGCGGCGAGTTCGTACCCCTTTCCCCC 960
DB 1248 GGAAGATGCTACAGAACAAATCCAGGAGGAGGCGGCGAGTTCGTACCCCTTTCCCCC 1307
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAAT 1367
QY 1021 TTTTATTTATTCATTAAGGTTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAAT 1080
DB 1368 TTTTATTTATTCATTAAGGTTAAGTGGGGGCTTTTAAAGTAAATTAATTAATTAATTAAT 1427
QY 1081 ATACATGTTTACACGATATTTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1140
DB 1428 ATACATGTTTACACGATATTTGTTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1487
QY 1141 GAGGCTACGTTGTTTACATTTTCCAGCAGTGTGTAGTCTCAGCAGCAGCTGTTCTTTT 1200
DB 1488 GAGGCTACGTTGTTTACATTTTCCAGTGTGTAGTCTCAGCAGCAGCTGTTCTTTT 1547
QY 1201 GTTGTGTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1260
DB 1548 GTTGTGTTGTTGGAAGTAAATCAATAGTGAATCTAGGACAGGTTTGGGGGTAAAGTACCG 1607
QY 1261 GGAGTGTAGGAGAGGGGCTGGTGTATGTTATGGTGGGGGAGGAGTAGTTTACATAGGGGTC 1320
DB 1608 GGAGTGTAGGAGAGGGGCTGGTGTATGTTATGGTGGGGGAGGAGTAGTTTACATAGGGGTC 1667
QY 1321 ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAAATTAACAGACTGAGGCC 1380
DB 1668 ATAGGTGAGGGCTGTGGCTTTGTTTACAAAGTTATCATCTAGAAATAACAGACTGAGGCC 1727
QY 1381 CACTCCCTCTGACCCCTGGGTGATCGGGGAGCAGGGCCAG 1420
DB 1728 CACTCCCTCTGACCCCTGGGTGATCGGGGAGCAGGGCCAG 1767
```

RESULT 14  
AA35381  
ID AAX35381 standard; DNA; 1768 BP.  
XX  
XX  
AC AAX35381;  
XX  
XX 07-JUL-1999 (first entry)  
XX  
XX Nucleotide sequence of PCV isolate Imp1010.  
DE  
XX PCV isolate; type II porcine circovirus; PCV; PMWS;  
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
XX Porcine circovirus.  
OS  
XX WO9918214-A1.  
XX  
XX 15-APR-1999.  
XX  
XX 01-OCT-1998; 98WO-FR002107.  
XX  
XX 03-OCT-1997; 97ER-00012382.  
XX  
XX 22-JAN-1998; 98FR-0000873.  
XX  
XX 20-MAR-1998; 98FR-00003707.  
XX  
XX (MERI-) MERIAL.  
XX  
XX (UYBE-) UNIV QUEBENS BELFAST.  
XX  
XX (UYSA-) UNIV SASKATCHEWAN.  
XX  
XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Haseard L;  
PI Harding J, Charreyre CE, Chappuis GE;  
XX  
XX WPI; 1999-264024/22.  
XX  
XX New type II porcine circovirus.  
XX  
XX Claim 11; Fig 4; 56pp; French.  
XX  
XX The present sequence represents the nucleotide sequence of PCV isolate  
CC Imp1010. The specification describes a preparation of type II porcine  
CC circovirus (PCV), which is particularly isolated from a lesion, from a  
CC pig with symptoms of PMWS (porcine multisystemic wasting syndrome). PCV  
CC (attenuated or inactivated); polypeptides derived from it, and vectors  
CC that express these polypeptides are all useful in vaccines, suitable for  
CC administration to adult or young pigs, or to pregnant sows (for passive  
CC immunization of their offspring). DNA isolated from PCV is used for in  
CC vivo or in vitro expression of viral polypeptides, also as probes or  
CC primers for diagnosis in usual hybridization or amplification assays.  
CC These polypeptides may also be used diagnostically to detect PCV-specific  
CC antibodies, while antibodies raised against the polypeptides can be used  
CC to detect antigens, in any usual immunoassay format  
XX  
XX Sequence 1768 BP; 451 A; 361 C; 495 G; 461 T; 0 U; 0 Other;  
SQ  
Query Match 75.6%; Score 1335.4; DB 2; Length 1768;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 1374; Conservative 0; Mismatches 46; Indels 1; Gaps 1;  
QY 1 ACCAGCGCACTTCGGCAGCGGCGGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCAGCA 60  
DB 348 ACCAGCGCACTTCGGCAGCGGCGGAGCACCTCGGCGAGCACCTCAGCAGCAACATGCCAGCA 407  
QY 61 AGAAGAAATGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTTCACCTCTGAATATC 120  
DB 408 AGAAGAAATGAAGAGCGGACCCCAACCCCAATAAAGGTGGGTTCACCTCTGAATATC 467  
QY 121 CTTCCGAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTA 180  
DB 468 CTTCCGAGACGAGCCGCAAGAAATACGGGATCTTCCAATATCCCTATTGATTATTTA 527  
QY 181 TTGTTGGCGAGGAGGGTAATGAGGAGGAGCAACCTCCTCCAGGGGTTCGCTAATT 240

DB 528 TTGTTGGCGAGGAGGGTAATGAGGAGGAGCAACCTCCTCCAGGGGTTCGCTAATT 587  
QY 241 TTGTTGAGGAGCAGACTTTTAAATAAGTGAAGTGTATTTGGGTCCCGCTCCACATCG 300  
DB 588 TTGTTGAGGAGCAAACTTTTAAATAAGTGAAGTGTATTTGGGTCCCGCTCCACATCG 647  
QY 301 AGAAGCGAAAGGAAACAGATCAGCAGAAATAAAGAAATCTGCACTAAAGAGCAACTTAC 360  
DB 648 AGAAGCGAAAGGAACTGATCAGCAGAAATAAAGAAATATTGCACTAAAGAGCAACTTAC 707  
QY 361 TGATGAGTGTGAGCTCCTAGATCTCAGGAGCAACGAGTGCACCTGTCTACTGTCTGCA 420  
DB 708 TTATTGAATGTGAGCTCCTCGATCTCAAGGAGCAACGAGTGCACCTGTCTACTGTCTG 767  
QY 421 GTACCTTGTGAGAGCGGAGTCTGGTGCACCGTGTGAGAGCAGCAGCCTCTGTAACGTTG 480  
DB 768 GTACCTTGTGAGAGCGGAGTCTGGTGCACCGTGTGAGAGCAGCAGCCTCTGTAACGTTG 827  
QY 481 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAGCGGAGAAATGCGAGAGCGTG 540  
DB 828 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAGTGAGCGGAGAAATGCGAGAGCGTG 887  
QY 541 ATTGGAAGACTAATGTACAGCTCACTTGTGGGCGCACCTGGGTGTGTAAGCAATGCG 600  
DB 888 ATTGGAAGACCAATGTACAGCTCACTTGTGGGCGCACCTGGGTGTGTAAGCAATGCG 947  
QY 601 CTGCTAATTTTGCAGACCGGAAACACATCTGGAACACCTAGTAAACAAAGTGTGGG 660  
DB 948 CTGCTAATTTTGCAGACCGGAAACACATCTGGAACACCTAGTAAACAAAGTGTGGG 1007  
QY 661 ATGTTTACCATGTGGAAGAGTGGTTTATTTGATGACATTTTATGCTGGCTGGCTGGG 720  
DB 1008 ATGTTTACCATGTGGAAGAGTGGTTTATTTGATGACATTTTATGCTGGCTGGCTGGG 1067  
QY 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATCTAGAGACTAAAGGTGGAAC 780  
DB 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTTGATCTAGAGACTAAAGGTGGAAC 1127  
QY 781 TACCTTTTGGCGCGCAGTATTCTGATTACCAAGCAATCAGACCCCGTTTGGAAATGTTACT 840  
DB 1128 TACCTTTTGGCGCGCAGTATTCTGATTACCAAGCAATCAGACCCCGTTTGGAAATGTTACT 1187  
QY 841 CCTCAACTGTGTCCAGCTGTGAGAGCTCTTTATCGGAGGATTAATCTCTGCTGGTATTT 900  
DB 1188 CCTCAACTGTGTCCAGCTGTGAGAGCTCTCTATCGGAGGATTAATCTCTGCTGGTATTT 1247  
QY 901 GGAAGATGTACAGAACCAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960  
DB 1248 GGAAGATGTACAGAACCAATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1307  
QY 961 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1020  
DB 1308 CATGCCCTGAATTTCCATATGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1367  
QY 1021 TTTTATTATTATTAAGG-TTAAGTGGGGGCTTTTAAATTAATTAATTAATTAATTAATTA 1079  
DB 1368 TTTTATTATTATTAAGGTTTAAAGTGGGGGCTTTTAAAGTAAATTAATTAATTAATTAATTA 1427  
QY 1080 CATACATGTTTACACGAGTATTGTTTCTGCTGCTATATCTATCTGTTTTCGAAACGAGTGC 1139  
DB 1428 CATACATGTTTACACGAGTATTGTTTCTGCTGCTATATCTATCTGTTTTCGAAACGAGTGC 1487  
QY 1140 CGAGGCTTACGTGTCTACATTTTCCAGAGTGTGTAGTCTCAGCAACAGTGTGTTCTTT 1199  
DB 1488 CGAGGCTTACGTGTCTCAGCATTTTCCAGAGTGTGTAGTCTCAGCAACAGTGTGTTCTTT 1547  
QY 1200 TGTGTTGTTGGAAGTAACTAATCTAGGAGAGGTTTCGGGTAAGTACC 1259  
DB 1548 TGTGTTGTTGGAAGTAACTAATCTAGGAGTCAAGAACAGGTTTGGGTGTGAAGTAC 1607  
QY 1260 GGGAGTGTAGGAGAGGCTGGCTTATGTTATCGCGGAGGAGTGTATTTACATAGGGGT 1319

Db 1608 GGGAGTGGTAGGAGAGGTTGGGGATTGTATGGCGGAGGAGTAGTTTACATATGGGT 1667  
Qy 1320 CATAGTGGAGGCTGTGCGCTTTGTTACAAAGTTATCATCTAAATAACAGCACTGGAGC 1379  
Db 1668 CATAGTTAGGCTGTGCGCTTTGTTACAAAGTTATCATCTAGATAACAGCAGTGGAGC 1727  
Qy 1380 CCATCCCTGTACCCCTGGGTGATCGGGGAGCAGGCCAG 1420  
Db 1728 CCATCCCTATCACCTGGGTGATGGGGAGCAGGCCAG 1768

## RESULT 15

AA35380  
ID AAX35380 standard; DNA; 1768 BP.  
XX  
AC AAX35380;  
XX  
XX  
DT 07-JUL-1999 (first entry)  
XX  
DE Nucleotide sequence of PCV isolate Imp999 (corrected version).  
XX  
XX PCV isolate; type II porcine circovirus; PCV; PMWS;  
KW porcine multisystemic wasting syndrome; pig; vaccine; ss.  
XX  
OS Porcine circovirus.  
XX  
XX WO918214-A1.  
XX  
XX  
PD 15-APR-1999.  
XX  
XX 01-OCT-1998; 98WO-FR002107.  
XX  
XX  
PR 03-OCT-1997; 97FR-00012382.  
PR 22-JAN-1998; 98FR-00000878.  
PR 20-MAR-1998; 98PR-00003707.  
XX  
XX (MERI-) MERIAL.  
PA (UYBE-) UNIV QUEENS BELFAST.  
PA (UYSA-) UNIV SASKATCHEWAN.  
XX  
XX Allan G, Meehan B, Clark E, Ellis J, Haines D, Haesard L;  
PI Harding J, Charreyre CE, Chappuis GE;  
XX  
XX WPI; 1999-264024/22.  
XX  
XX New type II porcine circovirus.  
XX  
XX  
XX Claim 11; Fig 3; 56pp; French.

CC The present sequence represents the nucleotide sequence of PCV isolate  
CC Imp999. The specification describes a preparation of type II porcine  
CC circovirus (PCV), which is particularly isolated from a lesion, from a  
CC pig with symptoms of PMWS (porcine multisystemic wasting syndrome). PCV  
CC (attenuated or inactivated), polypeptides derived from it, and vectors  
CC that express these polypeptides are all useful in vaccines, suitable for  
CC administration to adult or young pigs, or to pregnant sows (for passive  
CC immunization of their offspring). DNA isolated from PCV is used for in  
CC vivo or in vitro expression of viral polypeptides, also as probes or  
CC primers for diagnosis in usual hybridization or amplification assays.  
CC These polypeptides may also be used diagnostically to detect PCV-specific  
CC antibodies, while antibodies raised against the polypeptides can be used  
CC to detect antigens, in any usual immunoassay format

XX SQ Sequence 1768 BP; 453 A; 360 C; 494 G; 461 T; 0 U; 0 Other;

Query Match 75.6%; Score 1335.4; DB 2; Length 1768;  
Best Local Similarity 96.7%; Pred. No. 0;  
Matches 1374; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

Qy 1 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACTTCAGCAGCAATGCCCGCA 60  
Db 348 ACCAGCGCACTTCGGCAGCGGCGAGCACCTCGGCGAGCACTTCAGCAGCAATGCCCGCA 407

Qy 61 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGATATATC 120  
Db 408 AGAAGATGGAAGAGCGGACCCCAACCCCATATAAAGGTGGGTGTTCACTCTGATATATC 467  
Qy 121 CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCAATATCCCTATTTGATATTTTA 180  
Db 468 CTTCCGAAGACGAGCGCAAGAAATACGGGAGCTCCCNATCTCCCTATTTGATATTTTA 527  
Qy 181 TTGTTGGCGAGGAGGTAATGAGGAAGCAACCACTCAGCTCAGGGGTTCGTAATTT 240  
Db 528 TTGTTGGCGAGGAGGTAATGAGGAAGCAACCACTCAGCTCAGGGGTTCGTAATTT 587  
Qy 241 TTGTAAGAACGACACTTTTAAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300  
Db 588 TTGTAAGAACGACACTTTTAAATAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 647  
Qy 301 AGAAGCGAAAGGACAGATCAGCAGATAAAGAAATCTGCAGTAAAGCAACACTTAC 360  
Db 648 AGAAGCGAAAGGACAGATCAGCAGATAAAGAAATCTGCAGTAAAGCAACACTTAC 707  
Qy 361 TGATGGAGTGGAGCTCCTAGATCTCAGGACCAACCGAGTGACCTGTCTACTGTGTA 420  
Db 708 TTATTTGAATGTGGAGCTCCTCGATCTCAAGGACCAACCGAGTGACCTGTCTACTGTGTA 767  
Qy 421 GTACCTTTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTCTGAACGTTTG 480  
Db 768 GTACCTTTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTCTGAACGTTTG 827  
Qy 481 TCAGAAATTTCCGCGGGCTGCTGAACCTTTTGAAGTGCAGGGGAAATTCAGAGACGCTG 540  
Db 828 TCAGAAATTTCCGCGGGCTGCTGAACCTTTTGAAGTGCAGGGGAAATTCAGAGACGCTG 887  
Qy 541 ATTGGAAGACTAATGTACACGTCATTGTGGGCCCACTTGGGTGTTGTTAAAGCAAAATGGG 600  
Db 888 ATTGGAAGACCAATGTACACGTCATTGTGGGCCCACTTGGGTGTTGTTAAAGCAAAATGGG 947  
Qy 601 CTGCTAATTTTGCAGACCCGGAACCACTACTGAAACCACCTAGAAACAAGTGGTGG 660  
Db 948 CTGCTAATTTTGCAGACCCGGAACCACTACTGAAACCACCTAGAAACAAGTGGTGG 1007  
Qy 661 ATGGTTACCATGTTGAAGAAGTGGTGTATTATGATGACTTTTATGGCTGGCTGCCCTGG 720  
Db 1008 ATGGTTACCATGTTGAAGAAGTGGTGTATTATGATGACTTTTATGGCTGGCTGCCCTGG 1067  
Qy 721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 780  
Db 1068 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGTGGAACTG 1127  
Qy 781 TACCTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 840  
Db 1128 TACCTTTTGGCCCGCAGTATTCGATTAACAGCAATCAGACCCCGTGGAAATGGTACT 1187  
Qy 841 CCTCAACTGCTGCTCCAGCTGTAGAGCTCTTTATCGGAGGATTACTTCTTGGTATTTT 900  
Db 1188 CCTCAACTGCTGCTCCAGCTGTAGAGCTCTCTATCGGAGGATTACTTCTTGGTATTTT 1247  
Qy 901 GGAAGAATCTCAGAAACAATCCAGGAGGAAGGGGCGCAGTTGCTCACCTTTCCTCCCC 960  
Db 1248 GGAAGAATCTCAGAAACAATCCAGGAGGAAGGGGCGCAGTTGCTCACCTTTCCTCCCC 1307  
Qy 961 CATGCCCTGAATTTCCATATGAAATAAATACCTAGTCTTTTTTATCATTGCTGTAATGGT 1020  
Db 1308 CATGCCCTGAATTTCCATATGAAATAAATACCTAGTCTTTTTTATCATTGCTGTAATGGT 1367  
Qy 1021 TTTTATTTTCAATTAAGG-TTAAGTGGGGGCTTTAAATAAATTAATTTCTCTGAATTTGTA 1079  
Db 1368 TTTTATTTTCAATTAAGGTTAAGTGGGGGCTTTAAGATTAATAATTTCTCTGAATTTGTA 1427  
Qy 1080 CATACATGTTACACGGATATTGTATTCTCTGGTCGTATATCTGTTTTCGAAACGAGTGC 1139  
Db 1428 CATACATGTTACACGGATATTGTACTCTCTGGTCGTATATCTGTTTTCGAAACGAGTGC 1487  
Qy 1140 CGAGGCTACGTGGTCTACATTTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTCCTTT 1199

Db		CGAGCCCTACGTGTCACATTTCTAGAGTTTGTAGCCTCAGCCAAAGCTGATTCCTTT	1547
Qy		TGTTGTTTGGTTGGAAGTAATCAATAGTGAATCTAGGACAGGTTTGGGGTAAAGTACC	1259
Db		TGTTATTTGGTTGGAAGTAATCAATAGTGGAGTCAAGAACAGGTTTGGGTGTGAAGTAAC	1607
Qy		GGGAGTGTAGGAGAGGGCTGGGTTATGGTATGCGCGGAGGAGTAGTTTACATAGGGGT	1319
Db		GGGAGTGTAGGAGAGGGTTGGGGGATTGTATGCGCGGAGGAGTAGTTTACATATGGGT	1667
Qy		CATAGGTGAGGGCTGTGGCCCTTGTACAAAGTTTATCATCTAAATTAACAGCACTGGAGC	1379
Db		CATAGGTGAGGGCTGTGGCCCTTGTACAAAGTTTATCATCTAGATTAACAGCACTGGAGC	1727
Qy		CCACTCCCTCTCACCTGGGTGATCGGGGAGCAGGGCCAG	1420
Db		CCACTCCCTATCACCTGGGTGATGGGGGAGCAGGGCCAG	1768

Search completed: December 7, 2004, 17:57:13  
Job time : 880 secs